

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2004, 01:08:10 ; Search time 5838 Seconds
(without alignments)
3585.934 Million cell updates/sec

Title: JS-09-980-468-2
Perfect score: 2595
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Scoring table: BLOSUM62
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Ygapcp 10.0 , Ygapext 0.5
Fgapcp 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2	2595	100.0	2040	6	AX058830	AX058830 Sequence
3	2595	100.0	2040	8	CPU250734	AJ250734 Ceratodon
4	1619	62.4	2160	6	AX058840	AX058840 Sequence
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6	1475	56.8	1578	6	AX481617	AX481617 Sequence
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8	1475	56.8	2012	6	AX069275	AX069275 Sequence
9	1475	56.8	2012	8	PPAJ2980	AJ222980 Physcomit
10	1475	56.8	15430	6	AX481635	AX481635 Sequence
11	1475	56.8	15430	6	AX481964	AX481964 Sequence
12	1475	56.8	17752	6	AX481638	AX481638 Sequence
13	1475	56.8	17752	6	AX481967	AX481967 Sequence
14	1270	48.9	3518	8	PPAJ2981	AJ222981 Physcomit
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19	841.5	32.4	1617	6	AR098439	AR098439 Sequence
20	841.5	32.4	1617	6	AR136018	AR136018 Sequence
21	841.5	32.4	1617	6	AR215236	AR215236 Sequence
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SUMMARIES

ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO0075341.
ACCESSION AX058832
KEYWORDS AX058832.1 GI:12311152
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
1
REFERENCE
AUTHORS Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and
Zaehrer, U.
TITLE g(d)6-acetylenase and g(d)6-desaturase from ceratodon purpureus
JOURNAL Patent: WO 0075341-A 3 14-DEC-2000;
BASF AKTIENGESELLSCHAFT (DE)
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ORIGIN
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Pred. No.: 2595.00 Matches: 483
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Percent Similarity: 100.00% Mismatches: 0
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QY 481 HisAlaHis 483

Db 1450 CACGCTCAC 1458

RESJLT 2
AX058830
LOCUS
DEFINITION
AX058830
ACCESSION
AX058830.1 GI:12311150
VERSION
KEYWORDS
SOURCE
ORGANISM
Ceratonodon purpureus
Ceratonodon purpureus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratonodon.

REFERENCE
AUTHORS
Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and
Zaehrer, U.
TITLE
JOURNAL
Patent: WO 0075341-A 1 14-DEC-2000;
BASF AKTIENGESELLSCHAFT (DE)
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-09-980-468-2 (1-483) x AX058830 (1-2040)

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RESULT 3
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DEFINITION Ceratodon purpureus mRNA for delta 6-fatty acid acetylenase.
ACCESSION AJ250734
VERSION   AJ250734.1 GI:8670976.
KEYWORDS acetylenase; cytochrome b5; delta 6-fatty acid acetylenase.
SOURCE    Ceratodon purpureus
ORGANISM Ceratodon purpureus
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REFERENCE
AUTHORS   Sperling,P., Lee,M., Girke,T., Zahringer,U., Stymne,S. and Heinz,E.
TITLE      A bifunctional delta-fatty acyl acetylenase/desaturase from the
            moss Ceratodon purpureus. A new member of the cytochrome b5
            superfamily
JOURNAL   Eur. J. Biochem. 267 (12), 3801-3811 (2000)
MEDLINE   20307617
PUBMED    10848999
REFERENCE 2 (bases 1 to 2040)
AUTHORS   Sperling,P.
TITLE      Direct Submission
JOURNAL   Submitted (28-OCT-1999) Sperling P., Dept. Plant Physiology,
            Institut fuer Allgemeine Botanik, Universitaet Hamburg,
            Orkhorststrasse 18, D-22609 Hamburg, GERMANY
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LOCUS AX058840 2160 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 11 from Patent WO0075341.

ACCESSION AX058840
VERSION AX058840.1 GI:12311157
KEYWORDS
SOURCE Ceratodon purpureus

ORGANISM Ceratodon purpureus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.

REFERENCE 1
AUTHORS Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and
Zaehrer, U.
TITLE g(d)6-acetylase and -g(d)6-desaturase from ceratodon purpureus
JOURNAL Patent: WO 0075341-A 11 14-DEC-2000;
BASF AKTIENGESELLSCHAFT (DE)

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Qy	347	TrpAlaAlaPheHisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThr	366
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SOURCE	Physcomitrella patens		
ORGANISM	Physcomitrella patens		
REFERENCE			
AUTHORS	Heinz, E., Girke, T., Scheffler, J. and da Costa e Silva, O.		
TITLE	Plants expressing g(d)6-desaturase genes and oils from these plants containing pufas and method for producing unsaturated fatty acids		
JOURNAL	Patent: WO 0102591-A 1 11-JAN-2001;		
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QY	38	LysValSer	40
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QY	95	HisProGlyGlyThrValIleSerThrThrPheGlyArgAspGlyThrAspValPheAla	114
Db	727	CATCCCGGAGGATCAGTTATTATTATTTTGGACGAGACGGCACAGATGTTTCTCT	786
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DEFINITION        AX481635
ACCESSION          AX481635
VERSION            AX481635.1  GI:22316538
KEYWORDS           unidentified
SOURCE             unidentified
ORGANISM           unclassified.

REFERENCE
AUTHORS            Domergue,F., Zaehringner,U., Heinz,E., Renz,A. and Lerchl,J.
TITLE              Method for producing polyunsaturated fatty acids, novel
                    biosynthesis genes and novel plant expression constructs
JOURNAL            Patent: WO 02057465-A 25 25-JUL-2002;
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RESULT 14
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LOCUS

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DEFINITION Physcomitrella patens des6 gene.

ACCESSION AJ222981

VERSION AJ222981.1 GI:3790208

KEYWORDS delta6-acyl-lipid desaturase; des6 gene.

SOURCE Physcomitrella patens

ORGANISM Physcomitrella patens

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE 1

AUTHORS Girke,T., Schmidt,H., Zahringer,U., Reski,R. and Heinz,E.

TITLE Identification of a novel delta 6-acyl-group desaturase by targeted gene disruption in Physcomitrella patens

JOURNAL Plant J. 15 (1), 39-48 (1998)

MEDLINE 38416756

PUBMED 9744093

REFERENCE 2 (bases 1 to 3518)

AUTHORS Girke,T.

TITLE Direct Submission

JOURNAL Submitted (19-DEC-1997) Girke T., Institut fuer Allgemeine Botanik, Universitaet Hamburg, Chnhorststrasse 18, D-22609 Hamburg, GERMANY

FEATURES

Location/Qualifiers

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 20:19:04 ; Search time 7900 Seconds
(without alignments)
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Perfect score: 2040
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Scoring table: IDENTITY NUC
Gapop 10.0 ; Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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4	670	32.8	2160	6	AX058840	AX058840 Sequence
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12	567.4	27.8	17752	6	AX481638	AX481638 Sequence
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ACCESSION	AX058830.1	GI:12311150			
VERSION	AX058830.1				
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					

JOURNAL Patent: WO 0075341-A 1 14-DEC-2000;
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ORIGIN

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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CPU250734

LOCUS CPU250734 2040 bp mRNA linear PLN 21-JUN-2000

DEFINITION Ceratodon purpureus mRNA for delta 6-fatty acid acetylenase.

ACCESSION AJ250734

VERSION AJ250734.1 GI:8670976

KEYWORDS acetylenase; cytochrome b5; delta 6-fatty acid acetylenase.

SOURCE Ceratodon purpureus

ORGANISM Ceratodon purpureus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.

REFERENCE 1

AUTHORS Sperling,P., Lee,M., Girke,T., Zahringer,U., Stymne,S. and Heinz,E.

TITLE A bifunctional delta-fatty acyl acetylenase/desaturase from the moss Ceratodon purpureus. A new member of the cytochrome b5 superfamily

JOURNAL Eur. J. Biochem. 267 (12), 3801-3811 (2000)

MEDLINE 20307617

PUBMED 10848999

REFERENCE 2 (bases 1 to 2040)

AUTHORS Sperling,P.

TITLE Direct Submission

JOURNAL Submitted (28-OCT-1999) Sperling P., Dept. Plant Physiology, Institut fuer Allgemeine Botanik, Universitaet Hamburg, Charloersstrasse 18, D-22609 Hamburg, GERMANY

FEATURES

source location/Qualifiers

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3'UTR

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DB			
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DB			
QY	1921	GTTGGCAACACGAGTAGATCTAGTGTAATTTCTATTTCCGCAATGTAATATTACTCTGAA	1980
DB			
QY	1981	TATATACCGTTATCTATTTTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
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DB			

RESULT 3			
AX058832			
LOCUS	AX058832	1467 bp	DNA
DEFINITION	Sequence 3 from Patent WO0075341.		linear PAT 17-CAN-2001

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ACCESSION      AX058832
VERSION        AX058832.1  GI:12311152
KEYWORDS
SOURCE
  ORGANISM     Ceratodon purpureus
               Ceratodon purpureus
               Embryophyta; Streptophyta; Bryophyta;
               Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.

REFERENCE
  1. Heinze, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and
    Zaehrer, U.
    g(d)6-acetylenase and g(d)6-desaturase from ceratodon purpureus
    Patent: WO 0075341-A 3 14-DEC-2000;
    BASF AKTIENGESellschaft (DE)

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CDS

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RESULT 4

AX058840

LOCUS AX058840 2160 bp DNA linear PAT 17-JAN-2001

DEFINITION Sequence 11 from Patent WO0075341.

ACCESSION AX058840

VERSION AX058840.1 GI:12311157

KEYWORDS Ceratodon purpureus

SOURCE Ceratodon purpureus

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.

REFERENCE 1

AUTHORS Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and Zaehrer, U.

TITLE g(d)6-acetylase and g(d)6-desaturase from ceratodon purpureus

JOURNAL Patent: WO 0075341-A 11-14-DEC-2000;

FEATURES BASF AKTIENGESSELLSCHAFT (DE)

Location/Qualifiers

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Query Match 32.8%; Score 670; DB 6; Length 2160;

Best Local Similarity 69.8%; Pred. No. 1.1e-173;

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RESULT 5
CPU250735 2160 bp mRNA linear 21N 21-JUN-2000
LOCUS Ceratodon purpureus mRNA for delta 6-fatty acid desaturase.
DEFINITION AJ250735
ACCESSION
VERSION AJ250735.1 GI:8670978
KEYWORDS cytochrome b5; delta 6-fatty acid desaturase; desaturase.
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
REFERENCE 1
AUTHORS Sperling,P., Lee,M., Girke,T., Zahringer,U., Stymne,S. and Heinz,E.
TITLE A bifunctional delta-fatty acyl acetylase/desaturase from the moss Ceratodon purpureus. A new member of the cytochrome b5 superfamily
JOURNAL Eur. J. Biochem. 267 (12), 3801-3811 (2000)
MEDLINE 20307617
PUBMED 10848999

REFERENCE 2 (bases 1 to 2160)
AUTHORS Sperling,P.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1999) Sperling P., Dept. Plant Physiology, Institut fuer Allgemeine Botanik, Universitaet Hamburg, Ohnhorststrasse 18, D-22609 Hamburg, GERMANY
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3'UTR 1722..2142
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Query Match 32.8%; Score 670; DB 8; Length 2160;
Best Local Similarity 69.8%; Pred. No. 1.1e-173;
Matches 920; Conservative 0; Mismatches 395; Indels 3; Gaps 1;
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DB 1058 CACACCGATTGATGAGGATATTGATCTCTCCCATCATTTCTTGGAGTAAAGATCTCTT 1117
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DB 1655 CCGGTTTGGAAACACTTAAGGAGCTTGCCGATGCTGCTTCAACACGAGCCTTGCT 1712

RESULT 6
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LOCUS AX481617 1578 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 7 from Patent WO20057465.
ACCESSION AX481617
VERSION AX481617.1 GI:22316520
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1
AUTHORS Domergue, F., Zaehring, U., Heinz, E., Renz, A. and Lerchl, J.
TITLE Method for producing polyunsaturated fatty acids, novel
biosynthesis genes and novel plant expression constructs
JOURNAL Patent: WO 02057465-A 7 25-JUL-2002;

FEATURES
source BASF PLANT SCIENCE GMBH (DE)
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ORIGIN
Query Match 27.8%; Score 567.4; DB 6; Length 1578;
Best Local Similarity 66.3%; Pred. No. 2.5e-145;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;
QY 359 ACTTACTCTCTGGCCGATGTTGCTTCTCAGCAGCAGCCCTGGAGACTGCTGGATGATCGTC 418
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DB 730 CTGTGTTTCCAAACAGTCCGGATGGCTATCCCATGATTTTCTCCACAATCAGGTGTTTGAG 789
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DB 850 ACAGGCTGGTGGAGGAGGAGCAATACCTTCATCATGCTGCTCCAAATGAATCGGATCAG 909
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RESULT 7

AX481946

LOCUS AX481946 1578 bp DNA linear PAT 16-AUG-2002

DEFINITION Sequence 7 from Patent WO202057464.

ACCESSION AX481946

VERSION AX481946.1 GI:22316674

KEYWORDS Physcomitrella patens

SOURCE Physcomitrella patens

ORGANISM Physcomitrella patens

REFERENCE 1

AUTHORS Heinz, E., Duwenig, E., Bischoff, F., Drexler, H. and Lerchl, J. S.

TITLE Method for the expression of biosynthetic genes in plant seeds using novel multiple expression constructs

JOURNAL Patent: WO 02057464-A 7 25-JUL-2002;

FEATURES BASE PLANT SCIENCE GMBH (DE)

source 1.1578

location/Qualifiers

/organism="Physcomitrella patens"

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1.1578

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ORIGIN

Query Match 27.8%; Score 567.4; DB 6; Length 1578;

Best Local Similarity 56.3%; Pred. No. 2.5e-145;

Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

Qy 359 ACTTACTCTCTGGCGGATGTTGCTTCTCAGCACAGCCCTGGAGACTGCTGGAATGATGTC 418

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Db 373 AAAACAAGGTGTATGATGTTTCCAACTTTTGGGACGAGCATCCCGGAGGATCAGTTATT 429

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Qy 719 GCGACTATCTGTTACGACAAGATTACTTGGGCTATTGCTGTGTGAGCCAGTTTGTATGGGT 778

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DEFINITION	Sequence 1 from Patent WO0102591.		
ACCESSION	AX069275		
VERSION	AX069275.1	GI:12579151	
KEYWORDS			
SOURCE	Physcomitrella patens		
ORGANISM	Physcomitrella patens		
REFERENCE	Heinz, E., Girke, T., Scheffler, J. and da Costa e Silva, O.		
AUTHORS	Plants expressing g(d)6-desaturase genes and oils from these		
TITLE	plants containing pufas and method for producing unsaturated fatty acids		
JOURNAL	Patent: WO 0102591-A 1 11-JAN-2001;		
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	Query Match 27.8%; Score 587.4; DB 6; Length 2012;		
	Best Local Similarity 66.3%; Pred. No. 2.7e-145;		
	Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;		
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Db	868	CTGCTGAAAGATTTCGAGAAATGAGAGCTCTTTTCTGAGGAGCAACTTTTCAAAAGT	927
QY	659	TCCAAGGCTGTTCTGCTTCAGACTCTGATTAATGAGCTCTCTTTGCTGCGAGCATT	718
Db	928	TGAAATTTGACTATGTTATGAAGCTGCTCACGAATGTTGCTATTTTGTGCGAGCATT	987
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PPAJ2980

LOCUS PPAJ2980 2012 bp mRNA linear PLN 23-OCT-1998

DEFINITION Physcomitrella patens mRNA for delta6-acyl-lipid desaturase.

ACCESSION AJ222980

VERSION AJ222980.1 GI:3790206

KEYWORDS delta6-acyl-lipid desaturase; des6 gene.

SOURCE Physcomitrella patens

ORGANISM Physcomitrella patens

REFERENCE 1

AUTHORS Girke,T., Schmidt,H., Zahringner,U., Reski,R. and Heinz,E.

TITLE Identification of a novel delta 6-acyl-group desaturase by targeted gene disruption in Physcomitrella patens

JOURNAL Plant J. 15 (1), 39-48 (1998)

MEDLINE 98416756

PUBMED 9744093

REFERENCE 2 (bases 1 to 2012)

AUTHORS Girke,T.

TITLE Direct Submission

JOURNAL Submitted (19-DEC-1997) Girke T., Institut fuer Allgemeine Botanik, Universitaet Hamburg, Chorkorststrasse 18, D-22609 Hamburg, GERMANY

FEATURES

source

1 .2012

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ORIGIN

Query Match 27.8%; Score 567.4; DB 8; Length 2012;

Best Local Similarity 66.3%; Pred. No. 2.7e-145;

Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY 359 ACTTACTCTCTGCGCGATGTGCTTCTCAGCAGAGCGCTGGAGACTGCTGGATGATCGTC 418

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Db 1228 ACTTACCAACCAATTGATGAAGATATTGATACTCTCCCTCTCAITGCTGGAGCAAGGAC 1287

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RESULT 11
AX481964
LOCUS
DEFINITION
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VERSION
KEYWORDS
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AX481964
Sequence 25 from Patent WO02057464.
AX481964
AX481964.1 GI:22316692
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unclassified.
1
Heinz,E., Duwenig,E., Bischoff,F., Drexler,H. and Lerchl,J.S.
Method for the expression of biosynthetic genes in plant seeds
using novel multiple expression constructs
Patent: WO 02057464-A 25 25-JUL-2002;
BASF PLANT SCIENCE GMBH (DE)
Location/Qualifiers
1..15430
/organism="unidentified"
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AX481967

LOCUS

DEFINITION

AX481967

ACCESSION

AX481967

VERSION

AX481967.1 GI:22316695

KEYWORDS

SOURCE

ORGANISM

Heinz,E., Duwenig,E., Bischoff,F., Drexler,H. and Lerchl,J.S.

Method for the expression of biosynthetic genes in plant seeds

using novel multiple expression constructs

Patent: WO 02057464-A 28 25-JUL-2002;

BASF PLANT SCIENCE GMBH (DE)

Location/Qualifiers

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ACCESSION AX058834
VERSION AX058834.1 GI:12311154
KEYWORDS Ceratodon purpureus
SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
REFERENCE 1
AUTHORS Heinz,E., Stymne,S., Lee,M., Girke,T., Sperling,P. and
Zaehring,U.
TITLE g(d)6-acetylenase and g(d)6-desaturase from ceratodon purpureus
JOURNAL Patent: WO 0075341-A 5 14-DEC-2000;
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VERSION AX058836.1 GI:12311155
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SOURCE Ceratodon purpureus
ORGANISM Ceratodon purpureus
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REFERENCE 1
AUTHORS Heinz,E., Stymne,S., Lee,M., Girke,T., Sperling,P. and
Zaehring,U.
TITLE g(d)6-acetylenase and g(d)6-desaturase from ceratodon purpureus
JOURNAL Patent: WO 0075341-A 7 14-DEC-2000;
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Job time : 7910 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 20:15:54 ; Search time 818 Seconds
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ID	AAF25729	standard; DNA; 2040 BP.				
XX						
AC	AAF25729;					
XX						
DT	06-APR-2001	(first entry)				
XX						
DE	C. purpureus	delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 1.				
XX						
KW	Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;					
KW	transgenic plant; plant oil; triglyceride; nutrition; animal feed;					
KW	cosmetic; ds.					
XX						
OS	Ceratodon purpureus.					
XX						
FH	Key	Location/Qualifiers				
FT	CDS	176..1627				
FT		/*tag= a				
FT		/product= "delta6-acetylenase/delta6-desaturase"				
XX						
PN	WO200075341-A1.					
XX						
PD	14-DEC-2000.					
XX						
PF	07-JUN-2000; 2000WO-EP005274.					
XX						
PR	07-JUN-1999; 99DE-01025718.					
PR	22-DEC-1999; 99DE-01062409.					
XX						
PA	(BADI) BASF AG.					
XX						
PI	Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;					
XX						
DR	WPI; 2001-112150/12.					
DR	P-PSDB; AAB46435.					
XX						
PT	Nucleic acid encoding delta6-acetylenase or desaturase, useful for					
PT	producing plant oils with increased content of unsaturated fatty acids.					
XX						
XX	Claim 1a; Page 41-44; 69pp; German.					
XX						
CC	This invention describes a novel isolated nucleic acid (I) encoding					
CC	polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase					
CC	activity. The invention also describes (a) amino acid sequences encoded					
CC	by (I); (b) an expression cassette (EC) containing (I) linked to one or					

24	96	4.7	560	4	AAH05343	Aah05343 Human cDN
25	96	4.7	1335	4	AAD19403	Aad19403 Human del
26	96	4.7	1474	3	AAF21845	Aaf21845 Human bre
27	96	4.7	1575	6	ABL90108	Ab190108 Human pol
28	96	4.7	1686	2	AAV63641	Aav63641 Contig 25
29	96	4.7	1686	2	AAX00908	Aax00908 Human des
30	96	4.7	1686	2	AAV82640	Aav82640 Contig 25
31	96	4.7	1686	3	AAA14592	Aaa14592 Nucleotid
32	96	4.7	1686	3	AAA09451	Aaa09451 Human con
33	96	4.7	1686	3	AAA49937	Aaa49937 Human del
34	96	4.7	1686	6	ABS76711	Abs76711 Human des
35	96	4.7	1686	6	ABS71824	Abs71824 Human del
36	96	4.7	1843	2	AAV63642	Aav63642 Contig 25
37	96	4.7	1843	2	AAX00909	Aax00909 Human des
38	96	4.7	1843	2	AAV82641	Aav82641 Contig 25
39	96	4.7	1843	3	AAA14593	Aaa14593 Nucleotid
40	96	4.7	1843	3	AAA09452	Aaa09452 Human con
41	96	4.7	1843	3	AAA49938	Aaa49938 Human del
42	96	4.7	1843	6	ABS76712	Abs76712 Human des
43	96	4.7	1843	6	ABS71825	Abs71825 Human del
44	96	4.7	2146	4	AAH15815	Aah15815 Human cDN
45	96	4.7	2190	4	AAH16118	Aah16118 Human cDN


```
Db 1861 TCTATTCAGCGGCGATACGTACTAGTCCATATCGCGGTTGCCGAGATTACATTATTA 1920
QY 1921 GTGGGACACACGAGTAGATCTAGTGTAATTTCTATTTCCGCATGTAATATTACTCTGAA 1980
Db 1921 GTGGGACACACGAGTAGATCTAGTGTAATTTCTATTTCCGCATGTAATATTACTCTGAA 1980
QY 1981 TATATACCGTTATCTATTTCTTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 TATATACCGTTATCTATTTCTTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
```

RESULT 2

AAF25730 standard; DNA; 1467 BP.

XX AAF25730;

AC AAF25730;

XX

DT 06-APR-2001 (first entry)

DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 3.

XX

KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;

KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;

KW cosmetic; ds.

XX

OS Ceratodon purpureus.

XX

FH Key Location/Qualifiers

FT CDS 10. .1461

FT /*tag= a

FT /product= "delta6-acetylenase/delta6-desaturase"

XX

PN WO200075341-A1.

XX

PD 14-DEC-2000.

XX

PF 07-JUN-2000; 2000WO-EP005274.

XX

PR 07-JUN-1999; 99DE-01025718.

PR

PR 22-DEC-1999; 99DE-01062409.

XX

PA (BADI) BASF AG.

XX

PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;

XX

WPI; 2001-112150/12.

DR

DR P-PSDB; AAB46436.

XX

PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for

PT producing plant oils with increased content of unsaturated fatty acids.

XX

PS Claim 1a; Page 46-48; 69pp; German.

XX

CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
CC be used to suppress expression of (II), resulting in oils with increased
CC content of saturated fatty acids

XX

```
SQ Sequence 1467 BP; 356 A; 349 C; 379 G; 383 T; 0 U; 0 Other;
Query Match 71.4%; Score 1456.4; DB 4; Length 1467;
Best Local Similarity 39.9%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 171 CAAAAATGGCCCTCGTACCGACTTTCTGAACCTTTCTGGCAGCAGCATGGAGCAAGTACA 230
Db 5 CCAAAATGGCCCTCGTACCGACTTTCTGAACCTTTCTGGCAGCAGCATGGAGCAAGTACA 64
QY 231 GCGTGACACCCATAGCTATGCTGGAAGTATGCGGCTTCTTTGAAGCAGCCCAAAAGG 290
Db 65 GCGTGACACCCATAGCTATGCTGGAAGTATGCGGCTTCTTTGAAGCAGCCCAAAAGG 124
QY 291 TTTCTGCTCAAGGTAATACTCGGACAGACACTGAGACAGAGATCGGTGCAGGACAAA 350
Db 125 TTTCTGCTCAAGGTAATACTCGGACAGACACTGAGACAGAGATCGGTGCAGGACAAA 184
QY 351 AGCCAGGCACTTACTCTCGGCGGATGTTGCTTCTCAGCAGAGGCTTGAGACTGCTGGA 410
Db 185 AGCCAGGCACTTACTCTCGGCGGATGTTGCTTCTCAGCAGAGGCTTGAGACTGCTGGA 244
QY 411 TGATCGTCAAAGAGAAGGTGATGATATTAGCCGTTTTCGGACGACCACTCCTGGAGGGA 470
Db 245 TGATCGTCAAAGAGAAGGTGATGATATTAGCCGTTTTCGGACGACCACTCCTGGAGGGA 304
QY 471 CGGTAATTAGCACCTACTTTGGCGGGATGGCACAGACGTTTTCGCAACATTCATCCAC 530
Db 305 CGGTAATTAGCACCTACTTTGGCGGGATGGCACAGACGTTTTCGCAACATTCATCCAC 364
QY 531 CTGCCGCTGGAAGCACTCAATGACTACTACATTGGAGACCTTTGTAGGGAAGAGCCCC 590
Db 365 CTGCCGCTGGAAGCACTCAATGACTACTACATTGGAGACCTTTGTAGGGAAGAGCCCC 424
QY 591 TTGATGAATTGCTTAAAGACTACAGAGATATGAGAGCCGAGTTTGTAGAGAGGGCTTT 650
Db 425 TTGATGAATTGCTTAAAGACTACAGAGATATGAGAGCCGAGTTTGTAGAGAGGGCTTT 484
QY 651 TCAAGAGTTCGAAGGCTGTTCTGCTTCTGCTTCTGAGACTCTGATTAATGAGAGCTCT 710
Db 485 TCAAGAGTTCGAAGGCTGTTCTGCTTCTGAGACTCTGATTAATGAGAGCTCTCTTTG 544
QY 711 CGAGCATTCGACTATCTGTACGACAAAGAGTTACTGGCTTACTGTGCTGAGCCAGTT 770
Db 545 CGAGCATTCGACTATCTGTACGACAAAGAGTTACTGGCTTACTGTGCTGAGCCAGTT 604
QY 771 TGATGGGTCTCTTCGTCACAGTGTGGTGGCTTGCCTATGATTTCTTCAACACAGG 830
Db 605 TGATGGGTCTCTTCGTCACAGTGTGGTGGCTTGCCTATGATTTCTTCAACACAGG 664
QY 831 TCTTTGAGAACCGTACCGCGAATCTCTTCTTTGGCTATTGTTTCGGCAATTGCGTGTG 890
Db 665 TCTTTGAGAACCGTACCGCGAATCTCTTCTTTGGCTATTGTTTCGGCAATTGCGTGTG 724
QY 891 GCTTTAGTGTATCATGTTGGAGGACGAAGCAACATTCATCATCTGCTCCGAATGAGT 950
Db 725 GCTTTAGTGTATCATGTTGGAGGACGAAGCAACATTCATCATCTGCTCCGAATGAGT 784
QY 951 GCGACGAACAGTACACCTCTAGACGAAGACATTGATGATCTCTCCCATCATTTGCCTGGA 1010
Db 785 GCGACGAACAGTACACCTCTAGACGAAGACATTGATGATCTCTCCCATCATTTGCCTGGA 844
QY 1011 GCAAGGAAATTTTGGCCACCGTTGAGAGCAAGAGAAATTTGCGAGTGTCTCAATATCAG 1070
Db 845 GCAAGGAAATTTTGGCCACCGTTGAGAGCAAGAGAAATTTGCGAGTGTCTCAATATCAG 904
QY 1071 ACTACATGATTTCTGCTCTATTGTTTCATGGCCCGGTACAGTTGGACTTTTGGAGTTTGC 1130
Db 905 ACTACATGATTTCTGCTCTATTGTTTCATGGCCCGGTACAGTTGGACTTTTGGAGTTTGC 964
QY 1131 TCTTCACATTCAATCCTGATTTGAGCAGCAGCAAGGATTTGATAGAGAGGGAACAGTTG 1190
Db 965 TCTTCACATTCAATCCTGATTTGAGCAGCAGCAAGGATTTGATAGAGAGGGAACAGTTG 1024
```


Qy 899 GTATCATGTTGGAGGACGAAGCAACATTCATCATCTACTGCTCCGATGAGTGGACGAA 958
Db |||||
Qy 850 ACAGGTTGGTGAAGGAGGATTAACCTTCATCATGCTGCTCCAAATGAATGCGATCAG 909
Db |||||
Qy 959 CAGTACACACCTCTAGACGAAGACATTTGATATCTCTCCCATCATTTGCTGGAGCAAGGAA 1018
Db |||||
Qy 910 ACTTACCAACCAATTGATGAAGATATTGATATCTCTCCCATCATTTGCTGGAGCAAGGAC 969
Qy 1019 ATTTTGGCCACCGTTGAGAGCAAGAGAAATTTGCGAGTGTCTCAATATCAGCACTACATG 1078
Db |||||
Qy 970 ATACTGGCCACAGTTGAGAAATAGACATTTCTGGAATCTCTCAATACAGCATCTGTTC 1029
Qy 1079 ATTCTGCTCTATTGTTTCATGCGCCCGGTACAGTTGGACTTTTGGAAAGTTTCTCTTCACA 1138
Db |||||
Qy 1139 TTCAATCTCTGATTGAGCAACGACCAAGGATTTGATAGAGAGGAAACAGTTGCTTTTCAC 1198
Db |||||
Qy 1090 TCTACAGCAGTCTCTCACCTGTGACAGAGTTGTTGAGAGGGAAGTGTCTGTTTCAC 1149
Qy 1199 TACGCTGCTTCACTGCGGCTGCTTCCATATTTTSCCGGTTGCTGTAAGCCTCTTGGC 1258
Db |||||
Qy 1150 TACTTTGTTGTCGCGGACAGCGTGTATCTTCTCCCTGTT--TGAAGCCATTAGTA 1206
Qy 1259 TGGATGTTAGCAACTGAGCTTGTGGCGGTTTGTGTTGGGTTCTGTTTACGTTGAGT 1318
Db |||||
Qy 1207 TGGATGCGGTGACTGAGCTCATGTCGCAAGTCTGCTGGGCTTTGTATTTGACTTAGC 1266
Qy 1319 CACATGGAAGAGGAGTTTACATGATGAATCGAAGGACTTCTGTGAGAGCCAGCTTATTACC 1378
Db |||||
Qy 1267 CACATGGAAGGAGTTTATAATTCCTTAAGAAATTCGTGAGTGCACAGATCGTATACC 1326
Qy 1379 ACCGTTAACCAAGCGAGGCTGTTCAACGATTTGTTCACTGCGGAGTCTGACACCCAG 1438
Db |||||
Qy 1327 ACACGGATATCAAGGAACATATTAACGAGTGTTCACCTGTTGCTTAAACAGGCA 1386
Qy 1439 ATTGAGCATCACCTGTTTCCCAATGCCCCAGGCACAACTACCCCAAGATCGCACCTCAG 1498
Db |||||
Qy 1387 ATAGAGCATCATCTTTTCCCAACATGCCAGGCATAATTTAAACAAATAGCACCTAGA 1446
Qy 1499 GTCGAGGCTCTTTGCAAGAGCAGCGCTCGAGTACGATATGTTCTCGGTCGTTGCTGCC 1558
Db |||||
Qy 1447 GTGGAGTGTCTGTAGAAACACCGTCTGTTGACGAGACGATCTATTGCTACCGGC 1506
Qy 1559 TCTGTGCGGTTGTGAAGCGCTCAAGAAATTTGCTGATGAGCGTCAATTCGGCTT 1615
Db |||||
Qy 1507 ACTTCAAGGTTTGAAGCAATGAAGGAAGTCGCGGAGGCTGCGGAGAGCAGCAT 1563

RESULT 5
ABQ76782

ID ABQ76782 standard; cDNA; 1578 BP.

AC ABQ76782;

XX 25-MAR-2003 (first entry)

DE P. patens D6 desaturase cDNA SEQ ID 7.

XX Promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific; gene; ss.

XX Physcomitrella patens.

OS Key Location/Qualifiers

XX CDS 1..1578

FT /*tag= a

FT /product= "D6 desaturase"

PN DE10102338-A1.

XX

PD 25-JUL-2002.
XX 19-JAN-2001; 2001DE-01002338.
PF 19-JAN-2001; 2001DE-01002338.
XX 19-JAN-2001; 2001DE-01002338.
PR (BADI) BASF PLANT SCI GMBH.
XX Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
PI WPI; 2002-675961/73.
XX P-PSDB; ABG73602.
DR New expression cassette for plant genes, useful for preparing transgenic
XX plants that have increased production of polyunsaturated fatty acids.
PS Example 17; Page 64-67; 188pp; German.
XX This invention describes novel expression cassette (EC) containing at
CC least one each of plant promoter (P) and structural gene (SG) expressed
CC in plants, flanked by specific restriction enzyme (RE) recognition sites.
CC The EC has the structure (L1-P-SG-L2) n where L1 = is a polylinker
CC (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
CC sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
CC sequences and n = 1-3. The invention discloses a vector containing this
CC EC, an organism containing the EC or the vector and a transgenic plant
CC plants e.g linseed can be prepared with improved production of fatty acid
CC esters with an increased content of polyunsaturated fatty acids (PUFA),
CC useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
CC PUFA are known to reduce levels of cholesterol in the blood and to
CC protect against heart disease. The expression cassettes of the invention
CC provide increased and more efficient production of fine chemicals
CC (especially PUFA), including seed-specific production. This sequence
CC represents a nucleic acid sequence used to illustrate the method of the
CC invention
XX SQ Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 0 U; 0 Other;

Query Match 27.8%; Score 567.4; DB 6; Length 1578;

Best Local Similarity 66.3%; Pred. No. 3.8e-130;

Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

Qy 359 ACTTACTCTCTGGCGGATGTTGTTCTTCCACGACAGGCTGGAGACTGCTGGATCGTC 418
Db |||||
Qy 310 ACACACCCCTATCAGAAGTAGCAGTACACAAAGCCAGCGATTGCTGGATTGTTGA 369
Qy 419 AAAGAGAAGGTGTATGATATTAGCCCTTTTGGGACGACCCACCTGGAGGCGGTAATT 478
Db |||||
Qy 370 AAAACAAGGTGTATGATGTTTCCAAATTTTGGGACGAGCATCCCGGAGGATCAGTTATT 429
Qy 479 AGCACCCTACTTTGGCGGATGTCACACAGACGTTTTCGCAACATTCACCTCCACCTGCCGA 538
Db |||||
Qy 430 AGTACTTATTTTGGACGAGACGCGACAGATGTTTCTCTAGTTTTCATGACGCTTCTACA 489
Qy 539 TGGAAACCAACTCAATGACTACTATATTGGAGACCTTGTCTAGGGAAGAGCCCTTGTATGA 598
Db |||||
Qy 490 TGGAAATTTCTTCAAGACTTTTACATTTGGTGTGAGAGGGTGTGAGCCGACTCCAGAG 549
Qy 599 TTGCTTAAAGACTACAGAGATATGAGAGCCGAGTTTGTGTAGAGAGGGCTTTTCAAGAGT 658
Db |||||
Qy 550 CTGCTGAAAGATTTCGAGAAATGAGAGCTCTTTTCTCTGAGGAGCAACTTTTCAAAAGT 609
Qy 659 TCCAAGGCTGGTTCCTGCTTCAGACTCTGATTAATGACGCTCTCTTTGCTGCGAGCATT 718
Db |||||
Qy 610 TCGAAATGTACTATGTTATGAGAGCTGCTCAGCAATGTTGCTATTTTGTGCGAGCATT 669
Qy 719 GCGACTATCTGTACGACAGAGTACTTGGGCTATTGTGCTGTCAGCCAGTTTGTATGGGT 778
Db |||||
Qy 670 GCAATAATATGTTGGAGCAAGACTATTTCAGCGGTTTTCAGCGTTTGTATGATGGCT 729
Qy 779 CTCTTCGTCACAGTGTGGAGGCTTGCCCATGATTTTCTTTCATCAACAGGCTTTTGAG 838
Db |||||

QY	659	TCCAAGGCCTGGTTCCTGCTTCAGACTCTGATTAATGCAGCTCTCTTTGCTGCGAGCATT	718
Db	928	TCGAAATGTACTADGTTATGAAGCTGCTCACGAATGTGCTATTTTGTCTGCGAGCATT	987
QY	719	GCGACTATCTGTTACGACAAGAGTTACTGGGCTATTGTCTGTCTCAGCCAGTTTGATGGGT	778
Db	988	GCAATAATATGTTGGAGCAAGACTATTTTCAGCGGTTTGGCTTCAGCTTGATGATGGCT	1047
QY	779	CTCTTCGTCCTCCAAACAGTGTGATGGCTTGCCCATGATTTCTTCATCAACAGGCTTTTGAG	838
Db	1048	CTGTGTTTCCAAACAGTGGGATGGCTATCCCATGATTTTCTCCACAATCAGGCTTTGAG	1107
QY	839	ACCGGTACCGGGAACCTCTCTTTTGGCTATTTGTTCGGCAATTGCGTGTTCGCTTTAGT	898
Db	1108	ACACGCTGGCTTAAATGAAGTTGTCTGGGTATGTGATCGGCAACGCCGTTCTCGGGTTAGT	1167
QY	899	GTATCATGTGGAGGACGAAGCACCAACATTCATCATACTGCTCCGAATGATGGACGAA	958
Db	1168	ACAGGGTGTGGAAGGGAAGCATAAACCTTCATCATGCTGCTCCAAATGAATCGGATCAG	1227
QY	959	CAGTACACACCTCTTAGACGAAGACATTTGATACTCTCCCATCATTTGCCCTGAGCAAGAA	1018
Db	1228	ACTTACCAACCAATTTGATGAAGATATTGATCTCTCCCTCATTTGCCCTGGAGCAAGGAC	1287
QY	1019	ATTTTGGCCACCGTTGAGACGAAGAGAAATTTTGGAGTGCTTCAATATCAGCACTHCATS	1078
Db	1288	ATACTGGCCACAGTTGAGAATAAGACATTTCTTGGGATCCTCCAAATCCAGCATCTGTTTC	1347
QY	1079	ATTCTGCCTCTATTGTTTCATGGCCCGGTACAGTTGGACTTTTGGAGTTTGCTCTTCACA	1138
Db	1348	TTCATGGGCTCTGTTATTTTTCGCCCGTGGTAGTTGGCTCTTTTGGAGCTGGAGATATACC	1407
QY	1139	TTCAATCCTGATTTGAGCACGACCAAGGATTTGATGAGAAGGAACAGTTGCTTTTCAC	1198
Db	1408	TCTACAGCAGTGTCTCACCTGTTCGACAGGTTGTGAGAAAGGAACGTGTTCTGTTTCAC	1467
QY	1199	TACGCCCTGTTTCAGTTGGGCTGCTTCCATATTTTTCGGGTGTCGCTAAGCCTCTTGG	1258
Db	1468	TACTTTTGGTTCGTCGGACAGCGTGCTATCTCTCCCTGGT--TGGAGCCATTAGTA	1524
QY	1259	TGGATGGTAGCACTGAGCTTGTGGCCGGTTTCTGTGTTGGATTCGTGTTTACGTTGAGT	1318
Db	1525	TGGATGGCGGTGACTGAGCTCATGTCCGGCATGCTGCTGGGCTTTGTTTGTACTTAGC	1584
QY	1319	CACAATGGAAAGGAGSITTAACATGAATCGAAGACTTCGTGAGAGCCACGTTATTACC	1378
Db	1585	CACAATGGGATGGAGSITTAATAATTCGTCTAAAGAAATTCGTGATGCACAGATCGTATCC	1644
QY	1379	ACCCGTAACACCAAGCGAGGCTGGTTCAACGATTTGGTTTCACTGGGGGACTCGACACCCAG	1438
Db	1645	ACACGGGATATCAAGGAAACATATTTCAACGAGTGGTTCACTGGTGGCCTTAACAGGCAA	1704
QY	1439	ATTGAGCATCACCTGTTTCCAAACAATGCCAGGCACAACTACCCCAAGATCGCACCTCAG	1498
Db	1705	ATAGAGCATCATCTTTCCCAACAATGCCAGGCATATTTTAAACAAATAGCACCTAGA	1764
QY	1499	GTCGAGGCTCTTTGCAAGAAGCACCGCCTCGAGTACGTAATGTCTCCGTCGTTGGTGCC	1558
Db	1765	GTGGAGGTGTTCTGTAGAAACACGGTCTGGTGTACGAAGACGTATCTATTGCTACCGGC	1824
QY	1559	TCTGTCCGGGTTGTGAAGCGGCTCAAGGAAATTTGCTGATGAAGCGTCAATTGCGCTT	1615
Db	1825	ACTTGCAAGGTTTTGAAAGCATTTGAAGGAAGTCGCGGAGGCTGCGGCAGACAGCAT	1881

DT	28-MAR-2003	(first entry)
XX		
DE	Plant specific expression vector expressing desaturase SEQ ID NO 25.	
XX		
KW	Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;	
KW	animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;	
KW	plant; elongase; gene; ds.	
XX		
OS	Phaeodactylum tricornutum.	
OS	Physcomitrella patens.	
OS	Synthetic.	
OS	Chimeric.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	11543. .12415
FT		/*tag= a
FT		/product= "elongase"
FT		/note= "ABB98278"
FT		13313. .14890
FT	CDS	/*tag= b
FT		/product= "desaturase"
FT		/note= "ABB98277"
FT		

RESULT 8
ABV74274
ID ABV74274 standard; DNA; 15430 BP.
XX
XX ABV74274;
XX AC
XX
DT 07-AUG-2003 (revised)

SQ	Sequence	15430 BP; 3733 A; 3826 C; 4153 G; 3718 T; 0 U; 0 Other;
	Query Match	27.8%; Score 567.4; DB 6; Length 15430;
	Best Local Similarity	66.3%; Pred. No. 8.9e-130;
	Matches	833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;
QY	359	ACTTACTCTCTGCGCGATGTTGCTTCTCAAGCAGCGCTGGAGACTGCTGGATGACGTC 418
Db	13622	ACACACCCCTATCAGAAGTAGCAGTACACACACAGCGAAGCGATTGCTGGATTGTTGTA 13681
QY	419	AAAGAGAAAGGTGTATGATPATATAGCCGTTTTCGGACGACACCCCTGGAGGACGGTAATT 478
Db	13682	AAAAACAAGGTGTATGATGTTTCCAATTTCGGACGAGCATCCCGAGGATCAGTTATT 13741
QY	479	AGCACCTACTTTGGCGGAGTGGCAAGACGTTTTCGCAACATTCATCCACCTGCCGCA 538
Db	13742	AGTACTTATTTGGACGAGACGGCACAGATGTTTCTCTAGTTTTCATGCAGCTTCTACA 13801
QY	539	TGGAAGCAACTCAATGACTACTATACATTGGAGACCTTGCTAGGAGAGCCCTTGTATGAA 598
Db	13802	TGGAATAATTCTTCAAGACTTTTACATTGGTACCTGGAGAGGTGGAGCCGACTCCAGAG 13861
QY	599	TTGCTTAAAGACTACAGACATATGAGAGCCGAGTTTGTAGAGAGGGCTTTTTCAGAGT 658
Db	13862	CTGCTGAAGAGATTTCCGAGAAATGAGAGCTCTTTCCAGGAGCAACTTTTTCAGAGT 13921
QY	659	TCCAAGGCCTGTTCCCTGCTCAGACTCTGATTAATGAGCTCTCTTTGCTGGAGCACT 718
Db	13922	TCGAATTTGACTATGTTATGAAGCTGCTCAGCAATGTTGCTATTTTGTGCGAGCACT 13981
QY	719	GCGACTATCTGTTACGACAGAGTTACTGGGCTATTGCTGTGTCAGCCAGTTTGTAGGGT 778
Db	13982	SCAATAATATGTTGGAGCAAGACTATTTTCAGCGGTTTGGCTTCAGCTTGTATGATGGCT 14041
QY	779	CTCTTCGTCACACAGTGTGGATGGCTTGCCCATGATTTCCCTTCATCAACAGGCTTTTCAG 838
Db	14042	CTGTGTTTCCAACAGTGGCGATGGCTATCCCATGATTTTCTCCACAATCAGGTGTTTTCAG 14101
QY	839	ACCGGTACCGCGAACTCTTCTTGGCTATTTGTTGGCAATGTCGTGCTTGGCTTTAGT 898
Db	14102	ACACGCTGGCTTAATGAAGTTGTCGGGTATGTGATCGGCAACGCTTCTGGGGTTTGT 14161
QY	899	GTATCATGCTGGAGGACGAGCAACACATTCATCATATCTGCTCCGAATGAGTGGCAGCAA 958
Db	14162	ACAGGTTGTTGGAAGGAGAGCAATAACCTTCATCATGCTGCTCCCAATGAATGCGATCAG 14221
QY	959	CAGTACACACCTCTAGACGAGACATTTGATATCTCTCCCATCATTTGCTGGAGCAAGAA 1018
Db	14222	ACTTACCAACCAATTGATGAAGATATTGATACTCTCCCTCATTTGCTGGAGCAAGGAC 14281
QY	1019	ATTTTGGCCACCGTTGAGAGCAAGAGAAATTTTGGAGTGGTTCATATCAGCACTACATG 1078
Db	14282	ATACTGGCCACAGTTGAGATAAAGACATTTCTTGGCAATCCCTCAATACCAGCATCTGTT 14341
QY	1079	ATTTCTGCTCTATTGTTCTAGCCCGGTACAGTTGGACCTTTTGGAAAGTTTGTCTCTTACA 1138
Db	14342	TTTATGGGTCTGTTATTTTTCGCCCGTGGTAGTTGGCTCTTTTGGAGCTGGAGATATACC 14401
QY	1139	TTCAATCCTGATTTGAGCAGCAGCAAGGACTGTATAGAGAGGGAACAGTTGCTTTTAC 1198
Db	14402	TCTACAGCAGTCTCTCACCTGTTCAGACAGTTGTTGGAGAGGGAACAGTTCTGTTTTCAC 14461
QY	1199	TAGCCCTGTTTCTAGTTGGGCTGGCTTCCATATTTTGGCGGTGTCGCTAAGCCTCTTCG 1258
Db	14462	TACTTTTGGTTCTGTCGGACAGCGGTGCTATCTTCTCCCTGGT---TGAAGCCATTAG-A 14518
QY	1259	TGGATGGTAGCAACTGAGCTTGTGGCCGGTTTGTGTTGGGAATTCGTGTTACGTTGAGT 1318
Db	14519	TGGATGGCGGTGACTGAGCTCATGTCCGGCATGCTGCTGGGCTTGTATTGTTACTATAGC 14578
QY	1319	CACAATGGAAGGAGGTTTCAATGAATCGAAGGACTTCTGTGAGAGCCAGGTTATTACC 1378
Db	14579	CACAATGGGATGGAGGTTTATAATTCGCTCAAGAAATTCGTGAGTGCACAGATCGTATCC 14638

QY	1379	ACCGTAACACCAAGCGAGGCTGGTTCAACGATTGGTTCACTGGGGACTCGACACCCAG 1438
Db	14639	ACACGGGATATCAAGGAACATATTTCAACGACTGGTTCACTGGTGGCTTAACAGGCAA 14698
QY	1439	ATTGAGCATCACCTGTTTCCAAATGCCAGGCACTACCCAAAGATCGCACCTCAG 1498
Db	14699	ATAGAGCATCATCTTTTCCCAACAATGCCAGGCAATAATTTAAACAAAATAGCACCTAGA 14758
QY	1499	GTCCAGGCTCTTTGCAAGACGACGCGCTCGAGTACGATAATGTTCCGTCGTTGGTGCC 1558
Db	14759	GTGAGGCTGTTCTGTAAAGAAACACGGTCTGGTGTACGAAGACGTATCTATTGCTACCGGC 14818
QY	1559	TCTGTCGGGTTGTGAAGGCGCTCAAGGAAATTTGCTGATGAAGCGTCAATTCCGCTT 1615
Db	14819	ACTGCAAGGTTTGAAGCATTTGAAGGAAGTCGCGGAGGCTGCGGAGAGCAGCAT 14875
RESULT 10		
ABV74275		
ID	ABV74275	standard; DNA; 17752 BP.
XX	AC	ABV74275;
XX	DT	07-AUG-2003 (revised)
DT	28-MAR-2003	(first entry)
XX	XX	Plant specific expression vector expressing desaturase SEQ ID NO 28.
KW	Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;	
KW	animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;	
KW	plant; elongase; gene; ds.	
XX	OS	Phaeodactylum tricornutum.
OS	OS	Physcomitrella patens.
OS	OS	Synthetic.
OS	OS	Chimeric.
XX	PH	Key
FT	CDS	Location/Qualifiers
FT	FT	11543. .12415
FT	FT	/*tag= a
FT	FT	/product= "elongase"
FT	FT	/note= "ABB98273"
FT	FT	1313. .14890
FT	FT	/*tag= b
FT	FT	/product= "desaturase"
FT	FT	/note= "ABB98277"
FT	FT	15791. .17200
FT	FT	/*tag= c
FT	FT	/product= "desaturase"
FT	FT	/note= "ABB98274"
XX	PN	DE10102337-A1.
XX	PD	25-JUL-2002.
XX	XX	
PF	19-JAN-2001;	2001DE-01002337.
XX	PR	19-JAN-2001; 2001DE-01002337.
XX	PA	(BADI) BASF PLANT SCI GMBH.
XX	PI	Lerchl J, Renz A, Heinz E, Domerque F, Zaehrer U;
XX	XX	
DR	WPI; 2002-644810/70.	
DR	P-PSDB; ABB98278, ABB98277, ABB98274.	
XX	XX	Preparing ester containing polyunsaturated fatty acids, useful e.g. in
PT	animal or human nutrition, by transforming organism with desaturase gene	
PT	from: Phaeodactylum tricornutum.	
XX	XX	Example 11; Page 154-170; 182pp; German.
PS	XX	
XX	XX	

CC The invention relates to preparing (M1) fatty acid esters (II) with an
CC increased content of polyunsaturated fatty acids (II) with at least two
CC double bonds by introducing into a (I)-producing organism a specific
CC nucleic acid (A). (M1) is useful for preparing ester containing
CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
CC produced by (M1) are used in animal and human nutrition, cosmetics and
CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
CC the blood and to protect against heart disease. Cells that express (A)
CC are also used to identify (ant)agonists of desaturases, e.g. for
CC modulating the yield and rate of production of particular fine chemicals
CC in microorganisms (claimed). Also (A) and derived proteins can be used as
CC markers of specific genomic regions and in evolutionary/protein
CC structural studies. (M1) is suitable for large scale production (no known
CC bioengineering method can produce (II) on a useful scale). The present
CC sequence is that of the pUC19 based plant specific expression vector
CC (ABV74273) expressing the Physcomitrella patens elongase (ABB98278) and
CC the Phaeodactylum tricornutum desaturase (ABB98277 and ABB98274) of the
CC invention. (Updated on 07-AUG-2003 to correct OS field.)

SQ Sequence 17752 BP; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;

Query Match 27.8%; Score 567.4; DB 6; Length 17752;
Best Local Similarity 66.3%; Pred. No. 9.3e-130;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY 359 ACTTACTCTGCGCGATGTTGCTTCTCAGCAGCAGGCGCTGGAGACTGCTGGATCGTC 418
Db 13622 ACACACCCCTATCAGAGTAGCAGTACACAAAGCCAGCGATTGCTGGATTGTTGA 13681
QY 419 AAAGAGAGGTGTATGATATTAGCCGTTTCGGACGACACCCTGGAGGACGGTAATT 478
Db 13682 AAAACAAGGTGTATGATGTTTCCAAATTTTCGGACGAGCATCCCGGAGGATCAGTTATT 13741
QY 479 AGCACCCTACTTTGGCGGGGATGGCAGCAGCGTTTTCGCRACATTCCTCCACCTGCCGCA 538
Db 13742 AGTACTTATTTGGACGAGACGGCACAGATGTTTTCTTAGTTTTCAAGCAGCTTCTACA 13801
QY 539 TGAAGCAACTCAATGACTACTACATTGAGACCTTGCTAGGAGAGCCCTTGTATGAA 598
Db 13802 TGGAAATCTTCAAGACTTTTACATTGGTGACGTGGAGAGGGTGGAGCCGACTCCAGAG 13861
QY 599 TTGCTTAAAGACTACAGAGATATGAGAGCGAGTTTGTAGAGAGGGCTTTTCAAGAGT 658
Db 13862 CTGCTGAAAGATTTCCGAGAAATGAGAGCTCTTTTCTGAGGGAGCAACTTTTCAAAAGT 13921
QY 659 TCCAGGCGCTGCTGCTTTCAGACTCTGATTAATGACAGCTCTCTTGTCTGCGAGCAT 718
Db 13922 TCGAAATCTGACTATGTTATGAAGCTGCTCAGCAATGTTGCTATTTTGTCTGCGAGCAT 13981
QY 719 GCGACTACTGTTACGACAAGAGTTACTGGCTATTTGCTGTCTCAGCAGGTTTGTATGSGT 778
Db 13982 GCAATATATGTTGGAGCAAGACTATTTCAGCGGTTTGGCTTCAGTTGATGATGGCT 14041
QY 779 CTCTTCGTCCAAACAGTGTGGATGGCTTSCCCATGATTTCCTTCATCAACAGGCTTTTGAG 838
Db 14042 CTGTGTTCCAAACAGTGGGATGGCTATCCCATGATTTTCTCCACATCAGGTGTTTGAG 14101
QY 839 AACCGTACCGGGAACCTCTTCTTTGGCTATTGTTGGCAATTGCGTGCCTTGGCTTTAGT 898
Db 14102 ACACGCTGGCTTAATGAAGTTGTGGGATGATGATCGGCAACGCCGTTCTCGGGTTTAGT 14161
QY 899 GTATCATGGTGAGGACGAAGCAACAATTCATCATACTGCTCCGAATGATGCGACGAA 958
Db 14162 ACAGGGTGGTGAAGGAGAGCATAACTTCATCATGCTGCTCCAAATGAATGCGATCAG 14221
QY 959 CAGTACACACTCTAGACGAAGACATTGATACTCTCCCCATCAATTGCTGGAGCAAGGAA 1018
Db 14222 ACTTACCACCAATTTGATGAAGATATTGATGATCTCTCCCCCTCAATTGCTGGAGCAAGGAC 14281
QY 1019 ATTTTGGCCACCGTTGAGAGCAAGAGAAATTTTGGAGTGTCTCAATATCAGCACTACATG 1078
Db 14282 ATACTGGCCACAGTTGAGAAATAAGACATCTTTGGCAATCTCTCCATACCAGCATCTGTTT 14341

QY 1079 ATTCTGCCCTATATTGTTTCATGGCCCGGTACAGATTGGACTTTTGGAAAGTTTGTCTTCA 1138
Db 14342 TTCAATGGGCTGTTATTATTTTCGCCCGGTGTAGTGGCTCTTTTGGAGCTGGAGATATACC 14401
QY 1139 TTCAATCCCTGATTGAGCAGCAGCAAGGGATTGATAGAGAGGAAACAGTTGCTTTTCAC 1198
Db 14402 TCTACAGCAGTGTCTCTCACCTGTTCGACAGGTTGTGGAGAGGAACTGTCTGTTCAC 14461
QY 1199 TACGCCCTGTTGAGTTGGGCTGCGTTCCTCAATTTTCCGGGTGTCTGCTAAGCCTCTTGG 1258
Db 14462 TACTTTTGGTTCGTTCGGGACAGCGTGTCTCTCTCCCTGGT--TGGAGCCCATAGTA 14518
QY 1259 TGGATGGTAGCAACTGAGCTTGTGGCCGCTTGTGTTGGGATTGCTGTTTACGTTGAGT 1318
Db 14519 TGGATGGCGTGAAGTGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14578
QY 1319 CACAATGGAAAGGAGGTTTACCAATGAATCGAAGGACTTTCGTGAGAGCCCGGTTATTACC 1378
Db 14579 CACAATGGGATGAGGTTTATAATTGCTCTAAAGAAATTCGTGAGTGACAGATCGTATCC 14638
QY 1379 ACCCGTAAACCAAGCGAGGCTGTTTCAAGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1438
Db 14639 ACACGGGATATCAAGGAAACATATTTCAAGGACTGCTTCTGCTGCTGCTGCTGCTGCTGCT 14698
QY 1439 ATTGAGCATCACCCTGTTTCCCAACAATGCCAGGACAACTACCCCAAGATCGCACCTCAG 1498
Db 14699 ATAGAGCATCATCTTTTCCCAACAATGCCAGGCTAATTTAAACAATAAGCACCTAGA 14758
QY 1499 GTCGAGGCTCTTTGCAAGAAGCACGGCTTCAGTACGATATGCTCCGCTGCTGCTGCTGCT 1558
Db 14759 GTGAGGTTGTTCTGTAAAGAACACCGGCTTCGTGTACGAAGACGTTATCTATGCTACCGG 14818
QY 1559 TCTGTCGCGTGTGAAGCGGCTCAAGGAAATGCTGATGAAGCGTCAATTCGGCTT 1615
Db 14819 ACTTGCAAGGTTTGAAGGATTTGAAGGAACTGCGGAGGCTGCGGAGGCTGCGGAGCAGCAT 14875

RESULT 11

ABQ76797

ID ABQ76797 standard; DNA; 17752 BP.

XX AC ABQ76797;

XX DT 25-MAR-2003 (first entry)

XX DE pBARA1 encoding delta6 elongase, delta6 and delta5 desaturase.

XX KW Promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific; ds.

XX OS Physcomitrella patens.

OS OS Phaeodactylum tricornutum.

XX OS Synthetic.

Key	Location/Qualifiers
CDS	11543..12415
	/*tag= a
	/product= "delta6 elongase"
	/note= "from Physcomitrella patens"
CDS	13313..14890
	/*tag= b
	/product= "delta6 desaturase"
	/note= "from Physcomitrella patens"
CDS	15791..17200
	/*tag= c
	/product= "delta12 desaturase"
	/note= "from Phaeodactylum tricornutum"

XX DE10102338-A1.

PN 25-JUL-2002.

PD

XX PF 07-JUN-2000; 2000WO-EP005274.
XX PR 07-JUN-1999; 99DE-01025718.
XX PR 22-DEC-1999; 99DE-01062409.
XX PA (BADI) BASF AG.
XX PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX DR WPI; 2001-112150/12.
XX DR P-PSDB; AAB46437.
XX PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
XX PT producing plant oils with increased content of unsaturated fatty acids.
XX PS Example 6; Page 51; 69pp; German.
XX CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
CC be used to suppress expression of (II), resulting in oils with increased
CC content of saturated fatty acids
XX SQ Sequence 520 BP; 124 A; 116 C; 136 G; 144 T; 0 U; 0 Other;
Query Match 25.4%; Score 518.4; DB 4; Length 520;
Best Local Similarity 99.8%; Pred. No. 3.5e-118;
Matches 519; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 925 CATTTCATCATCTGCTCCGAATGAGTGGAGCAAGCAAGTACACACCTCTAGACGAGACAT 984
DB 1 CATTTCATCATCTGCTCCGAATGAGTGGAGCAAGCAAGTACACACCTCTAGACGAGACAT 60
QY 985 TGATACTCTCCCATCATCTGCTGGAGCAAGCAAGTATTTGGCCACCGTTGAGACGAGAG 1044
DB 61 TGATACTCTCCCATCATCTGCTGGAGCAAGCAAGTATTTGGCCACCGTTGAGACGAGAG 120
QY 1045 AATTTTGGAGTGCCTCAATATCAGCACTACATGATCTTGCCTCTATTGTTTCATGCGCCG 1104
DB 121 AATTTTGGAGTGCCTCAATATCAGCACTACATGATCTTGCCTCTATTGTTTCATGCGCCG 180
QY 1105 GTACAGTTGGACTTTTGGAAAGTTTGCCTCTTCAATCAATCCTGATTGAGCAGACCAA 1164
DB 181 GTACAGTTGGACTTTTGGAAAGTTTGCCTCTTCAATCAATCCTGATTGAGCAGACCAA 240
QY 1165 GGGATTGATAGAGAGGGAACAGTTGCTTTTCACTACGCTGTTTCACTGCTGCTGCTGCTG 1224
DB 241 GGGATTGATAGAGAGGGAACAGTTGCTTTTCACTACGCTGTTTCACTGCTGCTGCTGCTG 300
QY 1225 CCATATTTGCCGGTGTGCTGCTTAAAGCTCTTCCGTGGATGCTAGCAACTGAGCTTGTGSC 1284
DB 301 CCATATTTTGCCTGGTGTGCTGCTTAAAGCTCTTCCGTGGATGCTAGCAACTGAGCTTGTGSC 360
QY 1285 CGGTTTGTGTTGGATTGCTGTTTACGTTGAGTCAATGGAAGGAGGTTTACAATGA 1344
DB 361 CGGTTTGTGTTGGATTGCTGTTTACGTTGAGTCAATGGAAGGAGGTTTACAATGA 420
QY 1345 ATCGAAGGACTTCGTGAGAGCCAGGTTATTACACCGCTAACACCAAGCGAGGCTGTT 1404

DB 421 ATCGAAGGACTTCGTGAGAGCCAGGTTATTACACCCGTAACACCAAGCGGCTGTT 480
QY 1405 CAACGATTGTTCACTGGGGGACTCGACACCCAGATTGAG 1444
DB 481 CAACGATTGTTCACTGGGGGACTCGACACCCAGATTGAG 520
RESULT 13
AAF25732
XX ID AAF25732 standard; DNA; 514 BP.
AC AAF25732;
XX DT 06-APR-2001 (first entry)
XX DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 7.
XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
XX cosmetic; ds.
XX OS Ceratodon purpureus.
XX PN WO200075341-A1.
XX PD 14-DEC-2000.
XX PF 07-JUN-2000; 2000WO-EP005274.
XX PR 07-JUN-1999; 99DE-01025718.
XX PR 22-DEC-1999; 99DE-01062409.
XX PA (BADI) BASF AG.
XX PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX DR WPI; 2001-112150/12.
XX DR P-PSDB; AAB46438.
XX PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
XX PT producing plant oils with increased content of unsaturated fatty acids.
XX PS Example 6; Page 51; 69pp; German.
XX CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
CC be used to suppress expression of (II), resulting in oils with increased
CC content of saturated fatty acids
XX SQ Sequence 514 BP; 115 A; 113 C; 137 G; 149 T; 0 U; 0 Other;
Query Match 12.5%; Score 254.6; DB 4; Length 514;
Best Local Similarity 69.6%; Pred. No. 7.4e-53;
Matches 360; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
QY 925 CATTTCATCATCTGCTCCGAATGAGTGGAGCAAGCAAGTACACACCTCTAGACGAGACAT 984
DB 1 CATTTCATCATCTGCTCCGAATGAGTGGAGCAAGCAAGTACACACCTCTAGACGAGACAT 60

QY 985 TGATACTCTCCCATCATTCCTGCTGGAGCAAGGAATTTTGGCCACCCTTGGAGCAAGAC 1044
|||||
Db 61 TGATACTCTCCCATCATTCCTGCTGGAGCAAGGAATTTTGGCCACCCTTGGAGCAAGAC 120
|||||
QY 1045 AATTTTGGAGTGTCTCAATATCAGCACTACATGATTCGCTCTATTTGTTCAATGCTGCT 1104
|||||
Db 121 CATGTTGGAGTGTCTCAATATCAGCACTACATGATTCGCTCTATTTGTTGCTGCTGCTGCT 180
|||||
QY 1105 GTACAGTTGGACTTTTGGAGTGTCTCTTCAATATCAATCTGATTTGAGCAAGCAAA 1164
|||||
Db 181 GCGAGTTGGCTATTTTGGAGCGCGCTTCACTCTCAGGCGCGAGTTGACCTTGGCGA 240
|||||
QY 1165 GGGATTGATAGAGAGGGAACAGTTGCTTTTCACTACGCTGTTTCACTTGGCTGCTGCT 1224
|||||
Db 241 GAAGCTTTGGAGAGGGAACAGTTGCTTTTCACTACGCTGTTTCACTTGGCTGCTGCTGCT 300
|||||
QY 1225 CCATATTTGGCGGTTGCTGCTAAGCCTCTTGGCTGATGGTAGCAACTGAGCTTGTGGC 1284
|||||
Db 301 TATCTGCTCCCGG---ATGGAACACAGTTGTATGATGGTGTGCTCAGCGAGCTCATGTC 357
|||||
QY 1285 CGGTTTGTGTTGGGATTCGTTTACGTTGATGTCACATGGAAGGAGGTTTACAATGA 1344
|||||
Db 358 TGGTTTCTGCTGGGATACGTTATTTGATCTCAGTCACAATGGAATGGAGGTGTACAATAC 417
|||||
QY 1345 ATCGAAGGACTTCGTTGAGAGCCAGGTTATTACCAACCGTAACCAAGCGAGGCTGCTT 1404
|||||
Db 418 GTCAAAGGACTTCGTTGATGCTCCAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
|||||
QY 1405 CAACGATTGTTTCACTGGGGGACTCGACACCCAGATT 1441
|||||
Db 478 TAATGATTGTTTCAACCGAGGCTCTCAACAGACAGATT 514
|||||

RESULT 14

AAV63624
ID AAV63624 standard; cDNA; 1617 BP.

AC AAV63624;

XX 15-FEB-1999 (first entry)

DE cDNA encoding a delta-6 desaturase enzyme.

XX Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition;
KW inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes;
KW eczema; platelet aggregation; vasodilation; cholesterol level;
KW endometriosis; premenstrual syndrome; myalgic encephalomyelitis;
KW chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome;
KW hypertension; inflammatory skin disorder; ss.

XX Mortierella alpina.

XX Key Location/Qualifiers

FT CDS 71..1444

FT /*tag= a

FT /product= "delta-6 desaturase"

XX WO9846763-A1.

XX 22-OCT-1998.

PF 10-APR-1998; 98WO-US007126.

PR 11-APR-1997; 97US-00834655.

PA (CALJ) CALGENE LLC.

PA (ABBO) ABBOTT LAB.

PI Knutson D, Mukerji P, Huang Y, Thurmond J, Chaudhary S;
Leonard AE;

XX WPI; 1998-594582/50.

DR P-PSDB; AAW84137.

XX

PT New isolated fatty acid desaturase enzymes - used for the production of
PT polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions,
PT nutritional compositions, cosmetics or animal feed.

XX Claim 1; Fig 3A-E; 165pp; English.

CC The present sequence encodes a Mortierella alpina fatty acid delta-6
CC desaturase enzyme. The enzyme sequence is used in the methods of the
CC invention. The specification describes methods for desaturating a fatty
CC acid and for producing a desaturated fatty acid by expressing increased
CC levels of a desaturase. The present desaturase is an enzyme which
CC introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty
CC acid molecule. The enzyme can be used for desaturating fatty acids. The
CC enzyme can be used to produce polyunsaturated fatty acids, which can be
CC used for treating malnutrition, in pharmaceutical compositions, in
CC cosmetics or in animal feed. The polyunsaturated fatty acids can be used
CC for treating e.g. restenosis after angioplasty, inflammation, rheumatoid
CC arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood
CC pressure. They can also be used to inhibit platelet aggregation, cause
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
CC wall smooth muscle and fibrous tissue, reduce or prevent gastro-
CC intestinal bleeding and other side effects caused by non-steroidal anti-
CC inflammatory drugs, prevent or treat endometriosis and premenstrual
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral
CC infections, treat AIDS, multiple sclerosis, acute respiratory syndrome,
CC hypertension and inflammatory skin disorders

SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 U; 0 Other;

Query Match 7.5%; Score 153; DB 2; Length 1617;

Best Local Similarity 47.9%; Pred. No. 1.7e-27;

Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

QY 398 GGAGACTGCTGGATGATCGTCAAGAGAAGGTGTATGATATTAGCCGTTTTCGGACGAC 457
|||||

Db 158 GCACCCCTTCTTGATGATCATGACAACAAGGTGTACGATGTCGGAGTTCGTCCCTGAT 217
|||||

QY 458 CACCCCTGGAGGACGGTAATTAGCACCTACTTTGGCGGGGATGTCACAGACGTTTTCGCA 517
|||||

Db 218 CATCCCGGTGGAAGTGTGATTTCTCACGCACGTTTGGCAAGGACGACGCTCTTTGAC 277
|||||

QY 518 ACATTCATCCACCTGCGGATGGAAGCAACTCAATGACTACTATTCAGTGGAGACCTTGCT 577
|||||

Db 278 ACTTTTCAACCCGAGGCTGCTTGGGAGACTCTTSCCAACTTTTACGTTGGTGATATTGAC 337
|||||

QY 578 AGGGAAGAGCCC-----CTTGATGAATTTCTTAAAGACTACAGAGATATGAGAGCC 628
|||||

Db 338 GAGAGCGACCGCATATCAAGAATGATGACTTTTGGCGCGAGTTCGCAAGCTCGGTACC 397
|||||

QY 629 GAGTTTGTAGAGAAGGGCTTTTCAAGAGTTTCAAGGCTTGGTCTCTTCAGACTCTG 688
|||||

Db 398 TTGTTCCAGTCTCTTGGTTACTACGATCTTCCAAGGCATACGCTTCAAGGCTCTCG 457
|||||

QY 689 ATTAATGCAGCTCTC-----TTTGCTGCGAGCATTTGCGACTATCTGTACGACAAGAT 742
|||||

Db 458 TTCAACCTCTGCATCTGGGGTTTGTGACGGTTCATTGTGGCCAAGTGGGCCAGACCTCG 517
|||||

QY 743 TACTGGGCTATTGTGCTGTACGCCAGTTTGTATGGGTCTCTTCGTCCCAACAGTGTGGATGG 802
|||||

Db 518 ACCCTCGCCAACGTGCTCTGGGTGGGCTTTTGGGTCTGTTCGGCAGCAGTGGGATGG 577
|||||

QY 803 CTGCCCCATGATTTCTTCATCAACAGGTCTTTGAGAACCGTACCGGAACCTCTCTTT 862
|||||

Db 578 TTGGCTCACGACTTTTTCATCACAGGTCTTCCAGGACCGTTTCTGGGTGATCTTTTC 637
|||||

QY 863 GGCATTTGTTGGCAATTGGGTGCTTGGCTTTAGTGATCATGTTGAGGACGACGAC 922
|||||

Db 638 GCGGCTTCTTGGAGGTGTCTGCCAGGGCTTCTCGTCTCTGTTGGTGGAGGACAGCAC 697
|||||

QY 923 AACATTCATCATCTGCTCCGAATGAGTGCAGCAACAGTACACACCTCTAGACGAGAC 982
|||||

Db 698 AACACTCACACGCGCGCCCCAACGTTCCAGGAGGATCCCGACATTGACACCCACCT 757
|||||

QY 983 ATTGATACTCTCCCATCATTTGCTGGAGCAAGAAATTTGGCCACCGTTGAGAGCAAG 1042
|||
Db 758 CIGTTGACCTGGAGTGAGCATGCGTTGGGATGTTCTCGATGTCCAGATGAGGAGCTG 817
|||
QY 1043 AGAATTTTGGAGTGCTTCAATATCAGACTACATGATTTCTCTATTTGTTCAATGCTC 1102
|||
Db 818 ACCCGCATGTGCTGCGTTTCATGGTCTCGAACCAGACTGGTTTACTTCCCAATCTC 877
|||
QY 1103 CGGTACAGTTGGACTTTTGGAAAGTTTGCTCTTCACATTTCAAT----- 1144
|||
Db 878 TCGTTTGGCCGCTCTCTCTCGTGGTGGTCTCCAGTCCATTTCTTGTGCTGCTAAGGTCAG 937
|||
QY 1145 -----CCTGATTTGAGCACGACGACCAAGGATGATGAGAGGGAACAGTTGCT 1192
|||
Db 938 GCGCACAAAGCCCTCGGGCGCGGTGTGCCCCATCTCGTTGGTCGAGCAGCTGTGCTTGG 997
|||
QY 1193 TTTCACTACGCTGTGTTCAAGTTGGGCTGCTGCTTCCATATTTTCCGGGTGCTAAGCCT 1252
|||
Db 998 ATGCACTGGACCTGGTACCTGCGCACCATGTTTCCGTGTTTCATCAAGGATCCCGTCAACATG 1057
|||
QY 1253 CTTGCGTGGATGTTAGCACTGAGCTTGTGGCCGGTTTGTGTTGGGATTCGTTTACG 1312
|||
Db 1058 CTGGTGTACTTTTGGTGTGCGAGGCGGTGTGCGGAAACTTGTGGCGATCGTGTCTCG 1117
|||
QY 1313 TTGAGTCACAATGGAAGGAGGTTTACAATGAATCG-----AAGGACTTCTG 1360
|||
Db 1118 CTCACCAACAACGGTATGCTGTGATCTCGAAGGAGGAGGCGGTGATATGGATTCTTC 1177
|||
QY 1361 AGAGCCCGAGTTATTACCAACCGGTAAACACCAAGCGAGGCTGTTCAACGATTTGTTCACT 1420
|||
Db 1178 ACGAAGCAGATCATCAOGGTCGTGATGTCCACCCGGGTCTATTGTTGCAACTGTTTCAAG 1237
|||
QY 1421 GGGGGACTCGACACCCGAGATTGAGCATCACCTGTTTCCAAATGCCCCAGGCACACTAC 1480
|||
Db 1238 GGTGGATTGAATCTCAGATCGAGCACCACTTGTTCCTTCGATGCTCGCCCAACTTT 1297
|||
QY 1481 CCCAAGATCGACCTCAGTTCAGGCTCTTTGCAAGAGACAGCGGCTCGAGTACGATAAT 1540
|||
Db 1298 TCAAGATCCAGCTGCTGTCGAGACCTGTGTGCAAAAGTACAATGTCCGATACCACAC 1357
|||
QY 1541 GTCTCCGTGTTGGTCCCTCTGTGCGGTTGTGAAAGCGCTCAAGGAAATTCGTATGAA 1600
|||
Db 1358 ACCGGTATGATCGAGGGAACCTCGAGAGGTCTTTAGCCGTCTGAAAGAGGTCTCCAGGCT 1417
|||
QY 1601 GCGTCAATTCGGCTTCACGCTCACTAAGAAA 1631
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Db 1418 GCCTCCAAGATGGTAAAGCGCGAGTAAAAA 1448
|||

RESULT 15

AAAX00889
ID AAX00889 standard; DNA; 1617 BP.

AC AAX00889;

DT 26-MAR-1999 (first entry)

DE Mortierella alpina delta 6 desaturase encoding DNA.

XX Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
KW diabetes; cosmetic; animal feed; ss.

OS Mortierella alpina.

XX Key Location/Qualifiers

PH 71. .1443

FT /tag= a

FT /product= "delta 6 desaturase"

XX WO9846764-A1.
XX 22-OCT-1998.
XX 10-APR-1998; 98WO-US007421.
PF 11-APR-1997; 97US-00833610.
XX 11-APR-1997; 97US-00834033.
PR 11-APR-1997; 97US-00834655.
PR 24-OCT-1997; 97US-00956985.
XX (CALJ) CALGENE LLC.
PA (ABBO) ABBOTT LAB.
XX Knutzon D, Mukerji P, Huang Y, Thurmond J, Chaudhary S;
PI Leonard AE;
XX WPI; 1999-080739/07.
DR P-PSDB; AAW95504.
XX Nucleic acid construct able to express fatty acid desaturase in plants -
useful in human or animal nutrition, as cosmetics and therapeutically,
e.g. for restenosis, cancer and diabetes.
PS Claim 1; Fig 3A-B; 210pp; English.
XX This DNA encodes a Mortierella alpina delta 6 desaturase. The invention
relates to a nucleic acid construct that contains at least one of the
nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina delta 6,
delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively,
coupled to an expression control sequence functional in plants.
CC Recombinant plant cells containing at least one DNA encoding a M. alpina
fatty acid desaturase (FAD), can be used for the production of
CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
containing them are used to produce oils such as linoleic acid, or
CC arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid,
CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
CC dietary supplements or substitutes, for use in humans or animals; (iii)
CC for treating disorders associated with inadequate consumption or
CC production of PUFA (or their metabolites such as prostaglandins), e.g.
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
CC related coding sequences. Recombinant plants can produce high yields of
CC PUFA, since new pathways can be created and unwanted ones suppressed.
CC plants can be engineered to express oils of particular PUFA composition,
CC e.g. one similar to that in human milk, and product recovery is simpler
CC than with e.g. fish
XX SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 U; 0 Other;

Query Match 7.5%; Score 153; DB 2; Length 1617;
Best Local Similarity 47.9%; Pred. No. 1.7e-27;
Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

QY 398 GGAGACTGCTGGATGATCGTCAAGAGAGAGGTGTATGATATAGCCGTTTGGGACGAC 457
|||
Db 158 GCACCTTCTTGTATGATCATCGACAACAGGTGTACGATGTCGGGAGTTCGTCCTGAT 217
|||
QY 458 CACCTGAGGGACGGTAATTAGCACCTACTTTGGGGGGGATGGCACAGACGTTTTCGCA 517
|||
Db 218 CATCCCGTGAAGTGTGATTTCTCAGCACCGTGTGGCAAGAGCAGGACTGACGCTTTGAC 277
|||
QY 518 ACATTCCATCCACCTGCCGATGGAAGCAACTCAATGACTACTACATTGGAGACCTTGCT 577
|||
Db 278 ACTTTTCACCCCGAGGCTGCTTGGGAGACTCTTGGCAACTTTTACGTTGGTATATTGAC 337
|||
QY 578 AGGGAAGAGCCC-----CTTGATGAATTGCTTAAAGACTACAGAGATATGAGAGCC 628
|||
Db 338 GAGACGACCGCGATATCAAGAATGATGACTTTGGCGCCGAGGTCCGCAAGCTGCGTACC 397
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Search completed: June 18, 2004, 22:56:11
Job time : 829 secs

QY	629	GAGTTTGTAGAGAGGGCTTTTCAAGAGTTTCCAAGGCTGGTTCCTGCTTCAGACTCTG	688
Db	398	TTGTTCCAGTCTCTTGGTTACTACGATTCTTCCAAAGGCATACTACGCCCTTCAAGGTCTCG	457
QY	689	ATTAAATGCAGCTCTC-----TTTGCTGCGAGCATTTGGAGTATCTGTTCAGACAAGAGT	742
Db	458	TTCAACCTCTGCACTCTGGGTTTGTGACGGTCAATTGTGCCCAAGTGGGCCAGACCTCG	517
QY	743	TACTGGGCTATTGTGCTGTCAGCCAGTTTGAATGGTCTCTTCCGTCACACAGTGTGGATGG	802
Db	518	ACCTCGCCAAACGTTCTCGGCTGCGCTTTTGGGTCTGTCTGGCAGCAGTGGCGATGG	577
QY	803	CTTGCCCATGATTTCCTTCATCAACAGGTCCTTTGAGAACCGTACCCGAACTCCTTCTTT	862
Db	578	TTGGCTCAGCACTTTTTCATCACCAGGTCCTCCAGGACCGTTTCTGGGTGATCTTTTC	637
QY	863	GGCTATTGTTTCGGCAATTGGTGTCTTGGCTTTAGTGTATCATGGTGGAGGACGAGCAC	922
Db	638	GGCGCCTTCTTGGAGGTGTGTCCAGGGCTTCTCGTCTCTGTGGTGAAGGACAAGCAC	697
QY	923	AACATTCACTACTGCTCCGAATGAGTSCGACGAAACAGTACACACCTCTAGACGAAGAC	982
Db	698	AACACTCACACGCGCCGCCCAACGTCACGCGGAGGATCCGACATTGACACCCACCCT	757
QY	983	ATTGATACTCTCCCCATCATTGCTGGAGCAAGGAAATTTGGCCACCGTTGAGAGCAAG	1042
Db	758	CTGTTGACCTGGAGTGAGCATGCTGTGGAGATGTTCTCGGATGTCCAGATGAGGAGCTG	817
QY	1043	AGAAATTTSCGAGTGCCTTCATATCAGCACTACATGATCTGCTCTATTGTTCAATGGCC	1102
Db	818	ACCCGCATGTGGTCGGTTTCATGTCCTGAAACGACACCTGGTTTACTTCCCCATCTC	877
QY	1103	CGGTACASTTGGACTTTTGGAGTTTGTCTCTTCACATTCAAT-----	1144
Db	878	TCGTTTGGCCGTCTCTCTGCTGGTGCCTCCAGTCCATTCTCTTTTGTGCTGCCTAACGGTCTG	937
QY	1145	-----CCTGATTGACGACGACCAAGGGATTGATAGAGAAGGGAACAGTTGCT	1192
Db	938	GCCCCAAGCCCTCGGGCGCGGTGTGCCCCATCTCGTTGTCGACGAGCTGTGCTTGGG	997
QY	1193	TTTCACTACGCCCTGGTTCAAGTTGGGCTGCGTTCCATATTTTCCCGGTGTGCTAAGCCT	1252
Db	998	ATGCACTGGACCTGGTACCTCGCCACCATGTTCTCTGTTCATCAAGGATCCCGTCAACATG	1057
QY	1253	CTTGCGTGATGGTAGCACTGAGCTGTGGCCGGTTTGTGTTGGGATTCGTTGTTACG	1312
Db	1058	CTGGTGACTTTTGGTGTGCGAGGGGTGTGCGGAACTTGTGCGGATCGTGTCTCTCG	1117
QY	1313	TTGAGTCACAATGGAAGGAGGTTTACAATGAATCG-----AAGGACTTCGTG	1360
Db	1118	CTCAACCAACCGGTATGCCTGTGATCTCGAAGGAGGAGGGGTGATATGGATTCTTTC	1177
QY	1361	AGAGCCCGAGTTATTACCACCCGTAACACCAAGCGGCTGTTCAACGATTGTTCACT	1420
Db	1178	ACGAGCAGATCATCACGGGTGCTGATGTCCACCCGGGTCTATTGCCAACTGGTTCAAG	1237
QY	1421	GGGGACTCGACACCCAGATTGAGCATCACCTGTTTCCAACATGCCCCAGGCACAACTAC	1480
Db	1238	GGTGGATTGAACATATCAGATCGAGCACCACTTGTTCCTTCGATGCTCGCCACAACCTT	1297
QY	1481	CCAGATCGCACCTCAGGTGCGGCTCTTTGCAAGAAGCACGGCTCGAGTACGATAAT	1540
Db	1298	TCAAAGATCCAGCCTGCTGTGAGACCTGTGCAAAAAGTACAAATGTCCGATACCAACC	1357
QY	1541	GTCTCGGTGTTGGTGCCTCTGTGCGGTTGTGAAGGCGCTCAAGAAATGCTGATGAA	1600
Db	1358	ACCGGTATGATCGAGGGAACCTGCAGAGGTCTTTAGCCGCTGTAACGAGGTCTCCAAGGCT	1417
QY	1601	GCCTCAATTCGGCTTCACGCTCACTAAGAAA	1631
Db	1418	GCCTCAAGATGGGTAGGGCGAGTAAAAA	1448

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	7.5	1617	2	US-08-834-655-1
2	153	7.5	1617	3	US-08-834-033A-1
3	153	7.5	1617	3	US-09-363-574-1
4	153	7.5	1617	4	US-09-363-526-1
5	153	7.5	1617	4	US-09-330-235-17
6	96	4.7	1686	4	US-09-439-261-6
7	96	4.7	1686	4	US-09-227-613-6
8	96	4.7	1843	4	US-09-439-261-7
9	96	4.7	1843	4	US-09-227-613-7
10	96	4.7	2257	4	US-09-439-261-8
11	96	4.7	2257	4	US-09-227-613-8
12	96	4.7	2540	4	US-09-023-655-295
13	90.2	4.4	1362	4	US-09-769-863-13
14	87.6	4.3	1717	4	US-09-048-888-2
15	87.2	4.3	1684	2	US-08-831-570-1
16	87.2	4.3	1684	2	US-08-831-575-1
17	87.2	4.3	1685	1	US-08-366-779-4
18	87.2	4.3	1685	1	US-08-789-936-4
19	87.2	4.3	1685	4	US-08-934-254-4
20	87.2	4.3	1685	4	US-09-685-775-4
21	80.4	3.9	1478	4	US-09-148-545-63
22	80.4	3.9	2016	4	US-09-148-545-119
23	79.2	3.9	347	4	US-09-702-705-355
24	79.2	3.9	347	4	US-09-736-457-355
25	79.2	3.9	347	4	US-09-614-124B-355
26	79.2	3.9	347	4	US-09-671-325-355
27	79.2	3.9	347	4	US-09-589-184-355

28	79	3.9	449	4	US-09-439-261-38	Sequence 38, Appl
29	79	3.9	449	4	US-09-227-613-37	Sequence 37, Appl
30	79	3.9	473	4	US-09-439-261-37	Sequence 37, Appl
31	79	3.9	473	4	US-09-227-613-36	Sequence 36, Appl
32	79	3.9	655	4	US-09-439-261-3	Sequence 3, Appli
33	79	3.9	655	4	US-09-227-613-3	Sequence 3, Appli
34	79	3.9	864	4	US-09-439-261-12	Sequence 12, Appl
35	79	3.9	864	4	US-09-227-613-13	Sequence 13, Appl
36	79	3.9	1335	4	US-09-439-261-1	Sequence 1, Appli
37	79	3.9	1335	4	US-09-227-613-1	Sequence 1, Appli
38	79	3.9	1928	4	US-09-048-888-4	Sequence 4, Appli
39	62.8	3.1	1320	4	US-09-769-863-28	Sequence 28, Appl
40	51	2.5	1562	1	US-08-330-108-1	Sequence 1, Appli
41	51	2.5	1562	5	PCT-US92-10087-1	Sequence 1, Appli
42	50.8	2.5	19513	4	US-10-204-708-39	Sequence 39, Appl
43	50.6	2.5	593	4	US-09-904-615-59	Sequence 59, Appl
44	50.4	2.5	1413	4	US-09-769-863-19	Sequence 19, Appl
45	49.8	2.4	266	4	US-09-313-294A-3256	Sequence 3256, Ap

ALIGNMENTS

RESULT 1
US-08-834-655-1
; Sequence 1, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-655-1

Query Match 7.5%; Score 153; DB 2; Length 1617;
Best Local Similarity 47.9%; Pred. No. 3.7e-34;
Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

QY 398 GGAGACTGCTGGATGATCGTCAAAGAGAAGGTGTATGATATTAGCCGTTTTCGGAGCAG 457
Db 158 GCACCCCTTCTTGATGATCATCGACAACAAGGTGTACGATGTCGCGAGTTCGTCCTGAT 217
QY 458 CACCCCTGGAGGACGGTAATTAGCACCTACTTTGGGCGGGATGGCACAGACGTTTTCGCA 517
Db 218 CATCCCGGTGGAAGTGTGATTCACGCACCGTTGGCAAGGACGGCACTGACGTCCTTGAC 277
QY 518 ACATTCCATCCACCTGCCGCATGGAAGCAACTCAATGACTACTACATHTGGAGACCTTGCT 577
Db 278 ACTTTTCACCCCGAGGCTGCTTGGGAGACTCTTGCCAACTTTACGTTGGTGATATTGAC 337
QY 578 AGGGAAGAGCCC-----CTTGATGAATTGCTTAAAGACTACAGAGATATGAGAGCC 628
Db 338 GAGAGCGACCGCGATATCAAGAATGATGACTTTGGGCGGAGGTCCGCAAGTCCGTACC 397
QY 629 GAGTTTGTAGAGAGGGCTTTTCAAGAGTTCCAGGCTGCTGCTCCTGCTTCAGACTCTG 688
Db 398 TTSTTCCAGTCTCTTGTTACTACGATTCTTCCAGGCTACTACGCCCTTCAGGTCTCG 457
QY 689 ATTAATGCAGCTC-----TTTGCTGGAGCATTCGGACTATCTGTTACGACAAGAT 742
Db 458 TTCAACCTCTGCATCTGGGGTTTGTGCGAGGTCAATSTGGCCAAGTGGGGCCAGACCTCG 517
QY 743 TACTGGGCTATTGCTGTGTCAGCCAGTTTGTATGGTCTCTTCGTCGAACAGTGTGGATGG 802
Db 518 ACCCTCGCCAAACGTCCTCGGCTGCGCTTTTGGGTCGTTCTGCGCAGCAGTGGGATGG 577
QY 803 CTGCCCCATGATTCCTTCATCAACAGGTCCTTTCAGAACCGTACCGGAACTCCTTT 862
Db 578 TTGGCTCAAGACTTTTGCATCACAGGTCTTCCAGGACCGTTTCTGGGGTGATCTTTTC 637
QY 863 GGCTATTGTTCCGCAATTGCGTGTCTTGCTTTAGTGTATCATGTTGGAGGACGAGCAG 922
Db 638 GCGGCTTCTTGGAGGTGTCTGCCAGGCTTCTCGTCTCGTGTGGTGAAGGACAAGCAC 697
QY 923 AACATTCACTATCTGCTCCGAATGAGTGGCAGCAACAGTACACACCTCTAGACGAAGAC 982
Db 698 AACACTCACACCGCGCCGCCCAACGTCACCGGAGGATCCCGACATTGACACCCACCT 757
QY 983 ATTGATACTCTCCCCATCATTTGCTGGAGCAAGAAATTTGGCCACCGTTGACAGCAAG 1042
Db 758 CTGTTGACCTGGAGTGAGCATGCGTTGGAGATGTTCTCGGATGTCCAGATGAGGAGCTG 817
QY 1043 AGAATTTTGGAGTGTCTCAATATACAGCACTACATGATCTGCTCTATTGTTTCATGGCC 1102
Db 818 ACCCGCATGGGTGCGCTTTCATGTCCTGTAACCAAGACCTGGTTTACTTCCCATCTC 877
QY 1103 CGGTACAGTTGGACTTTTGGAAAGTTTGCTCTTCAANTCAAT----- 1144
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QY 1145 -----CCTGATTTGAGCACGACCAAGGATGATAGAGAAGGGAACAGTTGCT 1192
Db 938 GCGCACAGCCCTCGGCGCGCGTGTGCCCATCTCGTTGGTCGAGCAGCTGTGCTGCG 997
QY 1193 TTCACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1252
Db 998 ATGCATGGACCTGTTACCTCGCCACCATGTTCTCTTCATCAAGGATCCCGTCAACATG 1057
QY 1253 CTGCGTGGATGGTAGCACTGAGCTTGTGGCCGCTTGTGTTGGGATTCGTTTACG 1312
Db 1058 CTGGTGACTTTTGTGCTGCGAGGCGGTGTGCGGAAACTTGTGCGGATCGTGTCTCG 1117
QY 1313 TTGAGTCACAATGGAAGAGGTTTACATGATCG-----AAGGACTTCGTG 1363
Db 1118 CTCAACCAACACGGTATGCTGTGATCTCGAAGGAGGAGCGGTGCGATATGGAATTCCTC 1177
QY 1361 AGAGCCCAGGTTATTACACCCCGTAACACCAAGCGAGGCTGGTTCAACGATTTGGTTCACT 1420
Db 1178 ACGAAGCAGATCATCAGGTCGTGATGTCCACCCGCTCTATTGCGCAACTGTTTCAG 1237
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Db 1238 GGTGATTGAACATATCAGATCGAGCACCACCTTGTCCCTTCGATGCTCGCCACAACCTT 1297
QY 1481 CCCAAGATCGCACCTCAGTTCGAGGCTCTTTGCAAGAACGACGCGCTCGAGTACGATAAT 1540
Db 1298 TCAAAGATCCAGCCTGCTGTCGAGACCTGTGCAAAAAGTACAATGTCGATACCCACC 1357
QY 1541 GTCTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1600
Db 1358 ACCGGTATGATCGAGGAACTGCAGAGGTCTTTAGCCGCTGAAACGAGGTCTCCAGGCT 1417
QY 1601 GCGTCAATTGCGCTTCAGCTCACTAAGAAA 1631
Db 1418 GCCTCCAAGATGGTAAAGCGCAGTAAAAA 1448

RESULT 2
US-08-834-033A-1
; Sequence 1, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUITZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-834-033A-1

Query Match 7.5%; Score 153; DB 3; Length 1617;
Best Local Similarity 47.9%; Pred. No. 3.7e-34;
Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;
QY 398 GSAGACTGCTGGATGATCGTCAAAGAGAAGGTGTATGATATTAGCCGTTTTCGGAGCAG 457
Db 158 GCACCCCTTCTTGATGATCATCGACAACAAGGTGTACGATGTCGCGAGTTCGTCCTGAT 217
QY 458 CACCCCTGGAGGACGGTAATTAGCACCTACTTTGGGCGGGATGGCACAGACGTTTTCGCA 517
Db 218 CATCCCGGTGGAAGTGTGATTCACGACCGTTTGGCAAGGACGGCACTGACGTCCTTGAC 277

Db 338 GAGAGGACCGCGATATCAAGAAATGATGATCTTTGGCGCGAGGTCCGCAAGCTCGGTACC 397

Qy 625 GAGTTTGTAGAGAGGSGTTTCAAGAGTTCCAGGCGCTGGTTCTCTGCTTCAGACTCTG 688

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Qy 1145 -----CCTGATTTGAGCACGACCAAGGATGATAGAGAAAGGAAACAGTTGCT 1192

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Qy 1193 TTTCACTACGCTGTTTCACTGGCTGGCTGCTGCTTCCATATTTTCCGGTGTGCTTAAGCT 1252

Db 998 ATGCACTGGACCTGTTACTCGCCACCATGTTCTCTGTTTCATCAAGGATCCCGTCAACATG 1057

Qy 1253 CTGCGTGGATGGTAGCAACTGAGCTTGTGGCGGCTTGTGTTGGATTCGTTGTTACG 1312

Db 1058 CTGGTGACTTTTGTGTGCGAGGCGGTGTGCGGAACTTGTGGCGATCGTGTCTCG 1117

Qy 1313 TTGAGTCACAATGGAAGGAGGTTTACAATGAATCG-----AAGGACTTCGTG 1363

Db 1118 CTCACACCAACGGTATGCTGTGATCTCGAAGGAGGCGGTCGATATGGATTCTTTC 1177

Qy 1361 AGAGCCAGGTTATTACACCCGTAACACCAAGCGAGTGGTTCACAGATTGTTCACT 1423

Db 1178 ACGAAGCAGATCATCACGGTCTGATGTCCACCGGCTTATTGCCAACTGTTCACT 1237

Qy 1421 GGGGACTCGACACCCAGATGAGCATCACCTGTTTCCAAACAMGCCAGGCACTAC 1480

Db 1238 GGTGGATTGAACATATCAGATCGAGCACCACTTGTTCCTCTCGATGCTCGCCACAACTT 1297

Qy 1481 CCCAAGATCGCACCTCAGTTCGAGGCTCTTTGCAAGAGACACGGCTCGAGTACGATAAT 1540

Db 1298 TCAAGATCCAGCCTGCTTCGAGACCTGTGCAAAAAGTACAATGTCCGATACCACTC 1357

Qy 1541 GTCTCCGTTGGTGCCTCTGTGCGGTTGTGAAGSGCTCAAGGAAATTCGTGATGAA 1600

Db 1358 ACCGGTATGATCGAGGGAACCTGCAGAGGTCTTTAGCGCTCTGAACGAGGTCTCCAAGGCT 1417

Qy 1601 GCGTCAATTCGGCTTCACGCTCACTAAGAAA 1631

Db 1418 GCCTCCAGATGGGTAAAGCGCAGTAAAAAA 1448

RESULT 4

US-09-363-526-1

; Sequence 1, Application US/09363526

; Patent No. 6410288

; GENERAL INFORMATION:

; APPLICANT: KNUZON, DEBORAH

; APPLICANT: MURKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/363,526

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/DOCKET NUMBER: CGAB-201 USA

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1617 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

US-09-363-526-1

Query Match 7.5%; Score 153; DB 4; Length 1617;

Best Local Similarity 47.9%; Pred. No. 3.7e-34;

Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

Qy 398 GGAGACTGCTGGATGATCGTCAAGAGAAAGTGTATGATATAGCCGTTTTCGGGACGAC 457

Db 158 GCACCCCTTCTTGATGATCATGCAACAAGGTGTACGATGTCCGCGAGTTCGTCCTGAT 217

Qy 458 CACCCTGGAGGACGGTAATGACACCTACTTTGGCGGGATGGCACAGACGTTTTCGCA 517

Db 218 CATCCCGGTGAAGTGTGATCTCTCACGCACGTTTGGCAAGGACGCGACTGACGCTTTGAC 277

Qy 518 ACATTCCATCCACCTGCCGATGGAAGCAACTCAATGACTACTACATTGGAGACCTTGCT 577

Db 278 ACTTTTCACCCCGAGGCTGCTTGGGAGACTCTTGCCAACTTTTACGTTGGTGATATTGAC 337

Qy 578 AGGGAAGAGCCC-----CTTGATGAATTGCTTAAAGACTACAGAGATATGAGAGCC 628

Db 338 GAGAGCGACCGCGATATCAAGAATGATGACTTTGCGCGCGAGGTCCGCAAGCTGCGTACC 397

Qy 629 GAGTTTGTAGAGAGGCGCTTTTCAAGAGTTTCCAGGCTTCCAGGCTTCTGCTTCCAGACTCTG 688

Db 398 TTGTTCCAGTCTCTTGGTTACTACGATTCTTCCAGAGGACATACTACGCTTCAAGGTTCTCG 457

Qy 689 ATTAATGCAGCTCTC-----TTTGCTGGAGCAATTGGGACTATCTGTTACGACAGAGT 742

Db 458 TTCAACCTCTGCATCTGCGGTTTGTTCGACGGTCAATGTGGCCAAAGTGGGCCAGACCTCG 517
QY 743 TACTGGGCTATTGCTGTTCAGCCAGTTTGATGGTCTCTTCTCTCCAAACAGTGTGGATGG 802
Db 518 ACCCTCGCCAAACGTGTCTCGGCTGCGCTTTTGGGTCTGTCTTGGCAGAGTGGGATGG 577
QY 803 CTGCCCCATGATTTCTTCAACACAGGTCCTTGTAGAAACCGTACCGCGAACTCCTCTTT 862
Db 578 TTGGCTCAGCACTTTTGTGATCACCAGGTCTTCCAGGACCGTTTCTGGGGTGTATTTTC 637
QY 863 GGGTATTGTTCCGCAATTGCGTGTCTTGGCTTTTACTGTATCAGGTTGAGGACGAAGCAC 922
Db 638 GGGCGCTTCTTGGAGGTGTCTGCCAGGGCTTCTCGTCTCTGCTCGTGGTGAAGGACGAAGCAC 697
QY 923 AACATTCATCATCTGCTCCGAATGAGTGCAGCAGCAAGACAGTACACACCTCTAGACGAAGAC 982
Db 698 AACACTCACCAACGCGCCCCCAACAGCTCCACGGCGAGGATCCCGACATTTGACACCCACCT 757
QY 983 ATTGATACTCTCTCCCATCATTTGCCCTGGAGCAAGGAAATTTTGGCCACCGTTGAGAGCAAG 1042
Db 758 CTGTTGACCTGGAGTGAGCATGCGTTGGAGATGTTCTCGGATGTCCAGATGAGGAGCTG 817
QY 1043 AGAATTTTGGAGTGTCTTCAATATCAGCACTACATGATTTCTGCCCTCTATTGTTCAATGGCC 1102
Db 818 ACCCGCATGTGTGCGGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
QY 1103 CGGTACAGTTGGACTTTTGAAGTTTGTCTTCTTCAATCAATCAATCAATCAATCAATCAAT 1144
Db 878 TCGTTTGGCCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937
QY 1145 -----CCTGATTTGAGCAGCAAGGATTTGATGAGAGGATTTGATGAGAGGATTTGATGAGAGG 1192
Db 938 GCCCACAAGCCCTCGGCGCGCGTGTGCCCATCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 997
QY 1193 TTTCACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252
Db 998 ATGCACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057
QY 1253 CTGCGTGGATGGTAGCAACTGAGCTTGTGGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1312
Db 1058 CCGGTGATCTTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1117
QY 1313 TTGAGTCAAAATGGAAGGAGGTTTACAATGATGCTG-----AAGCACTTCTG 1360
Db 1118 CTCAACCAACAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1177
QY 1361 AGAGCCCAAGTTTATACCAACCGTAACACCAAGGAGGCTGCTTCAACGATTTGCTCACT 1420
Db 1178 ACGAAGCAGATCATCAACGCGTGTGATGTCCACCGGCTTATTTGCCAAGTGGTTCAG 1237
QY 1421 GGGGACTCGACACCCAGATTTGAGCATCACCTGTTTCCAAACATGCCAGGACCAACTAC 1480
Db 1238 GGTGGATTGAATATCAGATCGAGCACCCTTGTCTCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1297
QY 1481 CCCAAGATCGCACCTCAGGTCGAGGCTCTTTGCAAGAGCAGCGGCTCGAGTACGATAAT 1540
Db 1298 TCAAAGATCCAGCTGCTGCTGAGAGCCCTGTGCAAAAGTACAATGTCCGATACCAACC 1357
QY 1541 GTCTCCGTGCTTGGTGCCTCTGTGCGGCTTGTGAGGCGCTCAAGGAAATGCTGATGAA 1600
Db 1358 ACCGGTATGATCGAGGAACTGCAGAGGCTTTTAGCGCTGTGAACGAGGTCTCCAAAGGCT 1417
QY 1601 GCGTCAATTCGGTTTCACTGCTCACTAAGAAA 1631
Db 1418 GCCTCCAAGATGGGTAAGGCGCAGTAAAAA 1448

RESULT 5

US-09-330-235-17
; Sequence 17, Application US/09330235
; Patent No. 6459018
; GENERAL INFORMATION:

; APPLICANT: Knutzon, Debbie
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
; FILE REFERENCE: MOCO.156.00US
; CURRENT APPLICATION NUMBER: US/09/330,235
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/089,043
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Mortierella alpina
US-09-330-235-17

Query Match 7.5%; Score 153; DB 4; Length 1617;
Best Local Similarity 47.9%; Pred. No. 3.7e-34;
Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

QY 398 GGAGACTGCTGGATGATCGTCAAAGAGAAGGTGTATGATATTAGCCGTTTTCGGGACGAC 457
Db 158 GCACCCCTTCTTGATGATCATCGACAACAAGGTGTACGATGTCCGCGAGTTCGTCCCTGAT 217
QY 458 CACCCCTGGAGGACGGTAATTAGCACCTACTTTGGCGGAGTGGCACAGACGTTTTCGCA 517
Db 218 CATCCCGGTGGAAGTGTGATTTCTCACGCACGTTGGCAAGGACGACGCTGCTTTGAC 277
QY 518 ACATTCATCCACCTGCGCATGGAAGCAACTCAATGACTACTACTATTGGAGACCTTGTCT 577
Db 278 ACTTTTCAACCCCGAGGCTGCTTGGGAGACTCTTGCCAACTTTTACGTTGGTGATATTGAC 337
QY 578 AGGAAGAGGCCC-----CTTGATGAATTGCTTAAAGACTACAGAGATATGAGAGCC 628
Db 338 GAGAGCGACCGCGATATCAAGATGATGACTTTGCGGCGGAGGTCCGCAAGCTGCGTACC 397
QY 629 GAGTTTGTAGAGAAGGGCTTTTCAAGAGTTTCCAAGGCTGGTTTCTGCTTTCAGACTCTG 688
Db 398 TTGTTCCAGTCTCTTGGTTACTACGATTTCTTCCAAGGCACTACTAGCCCTTCAAGGTCTCG 457
QY 689 ATTAATGCAGCTCTC-----TTTGTCTGCGAGCAATTCGACTATCTGTTACGACAAGT 742
Db 458 TTCAACCTCTGCATCTGGGTTTGTGACGCTCAATTTGGCCAAAGTGGGCGCAGACCTCG 517
QY 743 TACTGGGCTATTGCTGTCTCAGCCAGTTTGTATGGTCTCTTCTGTCCTCAACAGTGTGGATGG 802
Db 518 ACCCTCGCCAAACGCTGCTCGGCTGCGCTTTGGGTCTGTCTGCGCAGCAGTGGGATGG 577
QY 803 CTGCCCCATGATTTCTTCAACAGGCTCTTTAGTGTATCATGTTGGAGGACGCAAGCAC 862
Db 578 TTGGCTCAGCACTTTTGCATCACCAAGGTCTTCCAGGACCGTTTCTGGGTGATCTTTTC 637
QY 863 GGCTATTGTTCCGCAATTCGCGCTTGGCTTTTAGTGTATCATGTTGGAGGACGCAAGCAC 922
Db 638 GGGCGCTTCTTGGGAGGTGTCTGCCAGGGCTTCTCGTCTCTGTTGGTGAAGGACGCAAGCAC 697
QY 923 AACATTCATCATCTGCTCCGAATGAGTGCAGCAGCAAGTACACACCTCTAGACGAAGAC 982
Db 698 AACACTCACCAACGCGCCCCCAACGTTCCACGGCGAGGATCCCGACATTTGACACCCACCT 757
QY 983 ATTGATACTCTCTCCCATCATTTGCCCTGGAGCAAGGAAATTTTGGCCACCGTTGAGAGCAAG 1042
Db 758 CTGTTGACCTGGAGTGAAGCATGCGTTGGAGATGTTCTCGGATGTCCAGATGAGGAGCTG 817
QY 1043 AGAATTTTGGAGTGTCTTCAATATCAGCACTACATGATTTCTGCCCTCTATTGTTCAATGGCC 1102
Db 818 ACCCGCATGTGTGCGGTTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
QY 1103 CGGTACAGTTGGACTTTTGAAGTTTGTCTTCTTCAATCAATCAATCAATCAATCAATCAAT 1144
Db 878 TCGTTTGGCCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937
QY 1145 -----CCTGATTTGAGCAGCAAGGATTTGATGAGAGGATTTGATGAGAGGATTTGATGAGAGG 1192

Dbb 938 GCCACAAAGCCCTCGGGGGGGTGTGCCCATCTCGTTGGTCGACGAGCTGTGCTTGGC 997
QY 1193 TTTCACTAGCCCTGGTTCACTGGGCTGCGTTCCTAATTTTGGCCGGTGTGCTAAGCCT 1252
Db 998 ATGCACTGGACCTGGTACCTCGCCACCATGTTCTTCTGTTCAATCAAGATCCCGTCAACTG 1057
QY 1253 CTTGGCTGGATGGTAGCAACTGAGCTGTGTGGCCGGTTTGTGTTGGGATTCGTGTTAAG 1312
Db 1058 CTGGTGTACTTTTGGTGTGCGAGGGGTGTGCGAAACTTGTGTCGATCGTTCTCG 1117
QY 1313 TTGAGTCAAAATGGAAGAGGAGTTTACAATGAATCG-----AAGGACTTCGTG 1360
Db 1118 CTCAAACCAACCGGTATCCCTGTGATCTCGAAGGAGGAGGCGGTGATATGGAATTTCTTC 1177
QY 1361 AGAGCCCAAGTTATTACCAACCGGTACACCAAGGAGGCTGTTCAACGATTTGTTCACT 1420
Db 1178 ACGAAGCAGATCATCAGGGTCTGTGATGTCCACCGGGTCTATTGCAACTGGTTCAAG 1237
QY 1421 GGGGGACTCGACACCCAGATTGAGCATCACCTGTTCCTCAACAATGCCAGGCACAACTAC 1480
Db 1238 GGTGGATGAACATATCAGATCGAGCACCACCTGTTTCCCTTCGATGCTCGCCACACTTT 1297
QY 1481 CCCAAGATCGACCTCAGGTCGAGGCTCTTTGCAAGAAGCAGCGCTCGAGTACGATAT 1540
Db 1298 TCAAAGATCCAGCCTGCTGTGAGACCCCTGTGCAAAAGTACAATGTCGATACCAACCC 1357
QY 1541 GTCTCCGTCGTGTTGGTCCCTCTGTGCGGGTGTGAAGGCGCTCAAGGAAATGCTGATGAA 1600
Db 1358 ACCGGTATGATCGAGGGAACCTGCAGAGGTCTTTAGCCGTCTGAACGAGGTCTCCAGGCT 1417
QY 1601 GCGTCAATCGGCTTCACGCTCACTAAGAAA 1631
Db 1418 GCCTCCAAGATGGGTAAAGGCGCAGTAAAAAA 1448

RESULT 6
US-09-439-261-6
; Sequence 6, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradipt
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-6

Query Match 4.7%; Score 96; DB 4; Length 1686;
Best Local Similarity 59.5%; Pred. No. 1.4e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;
QY 1292 TTGTTGGGATTCGTGTTTACGTTGAGTCACAATGGAAGGAGGTTTACAATGAATCGAA- 1350
Db 390 TGGTTTGTGGTCAACAGATGAATCACAATCGTCATGGAGATTGACGAGGAGGCTTAC 449
QY 1351 --GGACTTCGTGAGAGCCCGAGTTATTACCAACCGGTAAACCAAGCGAGGCTGTTCAAC 1408
Db 450 CGTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACGTTGGAGCAGTCTTCTTCAAC 509

QY 1409 GATTGGTTCACTGGGGGACTCGACACCCAGATTGAGCATCACTGTTTCCAAATGCCCC 1468
Db 510 GACTGGTTCACTGGGACACCTTAACCTTCCAGATTGAGCACCACCTCTTCCCACTATGCC 569
QY 1469 AGGCACAACTACCCCAAGATCGACCTCAGGTCGAGGCTCTTTGCAAGAAGCAGCGCCTC 1528
Db 570 CGGCACAACTTACACAAGATCGCCCGCTGTTGAAGTCTCTATGTGCCAAGCATGGCATT 629
QY 1529 GAGTACGATAATGTCTCCGTGCTGTTGGTGGCTCTGTGCGGTTGTGAAGCGCTCAAGGAA 1588
Db 630 GAATACCAAGGAGAGCCGCTACTGAGGCGCTGCTGGACATCATCAGTCCCTGAAGAAG 689
QY 1589 ATTG 1592
Db 690 TCTG 693
RESULT 7
US-09-227-613-6
; Sequence 6, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradipt
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-6

Query Match 4.7%; Score 96; DB 4; Length 1686;
Best Local Similarity 59.5%; Pred. No. 1.4e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;
QY 1292 TTGTTGGGATTCGTGTTTACGTTGAGTCACAATGGAAGGAGGTTTACAATGAATCGAA- 1350
Db 390 TGGTTTGTGGTCAACAGATGAATCACAATCGTCATGGAGATTGACGAGGAGGCTTAC 449
QY 1351 --GGACTTCGTGAGAGCCCGAGTTATTACCAACCGGTAAACCAAGCGAGGCTGTTCAAC 1408
Db 450 CGTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACGTTGGAGCAGTCTTCTTCAAC 509
QY 1409 GATTGGTTCACTGGGGGACTCGACACCCAGATTGAGCATCACCTGTTTCCAAATGCCCC 1468
Db 510 GACTGGTTCACTGGGACACCTTAACCTTCCAGATTGAGCACCACCTCTTCCCACTATGCC 569
QY 1469 AGGCACAACTACCCCAAGATCGACCTCAGGTCGAGGCTCTTTGCAAGAAGCAGCGCCTC 1528
Db 570 CGGCACAACTTACACAAGATCGCCCGCTGTTGAAGTCTCTATGTGCCAAGCATGGCATT 629
QY 1529 GAGTACGATAATGTCTCCGTGCTGTTGGTGGCTCTGTGCGGTTGTGAAGCGCTCAAGGAA 1588
Db 630 GAATACCAAGGAGAGCCGCTACTGAGGCGCTGCTGGACATCATCAGTCCCTGAAGAAG 689
QY 1589 ATTG 1592
Db 690 TCTG 693
RESULT 8
US-09-439-261-7
; Sequence 7, Application US/09439261
; Patent No. 6428990


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; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-7

Query Match      4.7%; Score 96; DB 4; Length 1843;
Best Local Similarity 59.5%; Pred. No. 1.4e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTTGGGATTCGTTTACGTTGAGTCACAATGGAAGGAGGTTTACAATGAATCGAA- 1350
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
547 TGGTTTGTGTGGTCCACACAGATGAATCAGATCGTCATGGAGHTTGACCCAGGAGGCTAC 606
QY 1351 --GGACTTCGTGAGAGCCCGAGGTTATTACCCCGTAACACCCAGCGAGGCTGGTTCAAC 1408
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
607 CGTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACCGTGGAGCAGTCCCTTCTTCAAC 666
QY 1409 GATTGGTTCACTGGGGGACTCGACACCCAGATTGAGCATCACCTGTTTCCAACAATGCC 1468
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
667 GACTGGTTCAGTGGACACCTTAACCTCCAGATTGAGCACCACCTCTTCCCACCATGCC 726
QY 1469 AGGCACAACTACCCCAAGATCGCACCTCAGGTCGAGGCTCTTTGCAAGAGCGCTCAAG 1588
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
727 CGGCACAACTTACACAGATCGCCCGCTACTGAGGCGCTGTTGAAGTCTCTATGTGCCAGCATGGCATT 786
QY 1529 GAGTACGATAATGTCTCCGTCGTTGGTGCTCTGTGCGGTTGTGAAGGCGCTCAAGGAA 1588
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
787 GAATACCAAGGAGAGCGCTACTGAGGCGCTGCTGACATCATCAGGTCCCTGAAGAAG 846
QY 1589 ATTG 1592
Db |||||
847 TCTG 850

RESULT 9
US-09-227-613-7
; Sequence 7, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-7

; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-8

Query Match      4.7%; Score 96; DB 4; Length 2257;
Best Local Similarity 59.5%; Pred. No. 1.6e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTTGGGATTCGTTTACGTTGAGTCACAATGGAAGGAGGTTTACAATGAATCGAA- 1350
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
961 TGGTTTGTGTGGTCCACACAGATGAATCAGATCGTCATGGAGATTGACCCAGGAGGCTAC 1020
QY 1351 --GGACTTCGTGAGAGCCCGAGGTTATTACCCCGTAACACCCAGCGAGGCTGGTTCAAC 1408
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1021 CGTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACCGTGGAGCAGTCCCTTCTTCAAC 1080
QY 1409 GATTGGTTCACTGGGGGACTCGACACCCAGATTGAGCATCACCTGTTTCCAACAATGCC 1468
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1081 GACTGGTTCAGTGGACACCTTAACCTCCAGATTGAGCACCACCTCTTCCCACCATGCC 1140
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```

; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-8

Query Match      4.7%; Score 96; DB 4; Length 2257;
Best Local Similarity 59.5%; Pred. No. 1.6e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 1292 TTGTTGGGATTCGTTTACGTTGAGTCACAATGGAAGGAGGTTTACAATGAATCGAA- 1350
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
961 TGGTTTGTGTGGTCCACACAGATGAATCAGATCGTCATGGAGATTGACCCAGGAGGCTAC 1020
QY 1351 --GGACTTCGTGAGAGCCCGAGGTTATTACCCCGTAACACCCAGCGAGGCTGGTTCAAC 1408
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1021 CGTGACTGGTTCAGTAGCCAGCTGACAGCCACCTGCAACCGTGGAGCAGTCCCTTCTTCAAC 1080
QY 1409 GATTGGTTCACTGGGGGACTCGACACCCAGATTGAGCATCACCTGTTTCCAACAATGCC 1468
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1081 GACTGGTTCAGTGGACACCTTAACCTCCAGATTGAGCACCACCTCTTCCCACCATGCC 1140
```



```

1 GENERAL INFORMATION:
2 APPLICANT: Abbott Laboratories
3 APPLICANT: Mukerji, Pradip
4 APPLICANT: Kuang, Yung-Sheng
5 APPLICANT: Das, Tapas
6 APPLICANT: Thurmond, Jennifer
7 APPLICANT: Pereira, Suzette L.
8 TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
9 FILE REFERENCE: 6763.US.01
10 CURRENT APPLICATION NUMBER: US/09/769,863
11 CURRENT FILING DATE: 2001-01-25
12 NUMBER OF SEQ ID NOS: 32
13 SOFTWARE: FastSEQ for Windows Version 4.0
14 SEQ ID NO 13
15 LENGTH: 1362
16 TYPE: DNA
17 ORGANISM: Saprolegnia diclina
18 US-09-769-863-i3

```

Query Watch	4.4%	Score 90.2;	DB 4;	Length 1362;
Best Local Similarity	47.4%;	Pred. No. 5.8e-16;		
Matches 429;	Conservative	0;	Mismatches 443;	Indels 33;
				Gaps 4;

QY	756	TGCTGT	CAGCCAGTTTGATGGGTCTCTTCGTC	CAACAGTGTGGATGGCTTGCCCATGATT	815
Db	458	TGGTCG	GGGCTGTATCTCTTGGCCTCTTTTAC	CASGATGCGGTGGCTCGCCCATGACT	517
QY	816	TCCTTCA	TCAACACGGTCTTTGAGAACCGTACCG	CGAATCTCTTTGGCTATTATTGTTCTG	875
Db	518	TTCTGCA	CCACCAAGTGTTTGAGAACCACTTGT	TTCCGACCTCGTCGGCGTCATGGTCG	577
QY	876	GCAATTG	CGTGCTTGGCTTTAGTGTATCATGGT	GAGGACGAAGCAACAATTCATCATATA	935
Db	578	GCAACCT	CTGCGAGGCTTCTCGGTG	CAGTGGTGAAGAACAGCAACAACGCA	637
QY	936	CTGCTCC	GAAAAATGAGTGGACGAACAGTACAC	ACTCTAGACGAAGACATTGTATA	989
Db	638	CGATCCCC	AACCTTCCACGGACGCCCGAGATCG	CCCTTCCACGGCGACCCGGACATTGACA	697
QY	990	CTCTCCCC	ATCATTTGCCGTG--GAGCAAGGAAT	TTTGGCCACCGTTGAGAGCAAGAGAA	1046
Db	698	CGATGCC	GAATCTTCGCTGGTTCGCTCAAGAT	GGCGAGCACGCGTTCGACTCGGCCGTCG	757
QY	1047	TTTTCG	AGTGCTCAATATCAGCACTACATGAT	TTCTGCCTCTATTGTTTCATGGCCCGGT	1106
Db	758	GGCTCT	CTTCTATCGCTACCAAGCGTACCT	GTACTTCCCATCTTGCTCTTTGCGCGTA	817
QY	1107	ACAGTTG	GAATTTGGAAGTTTGTCTCTTCA	ATTCAATCCTGATTTGAGCACGACCA--	1163
Db	818	TCTCGT	GGTGTATCCAGTCGGCCATGTAC	GCCTTCTACAACGTTGGGCCCGGCGACCT	877
QY	1164	-----	AGGGATTGATAGAGAAGGAACAG	TGTGCTTTTCACTACGCTGGT	1208
Db	878	TTGACA	AGSTCCAGTACCGCTGCTCG	AGCGGCGCGGCTCCTCCTCTACTAC	937
QY	1209	TCAGTTG	GGCTGCGTTCATATTTTCCGGG	STCGCTAAGCCTCTTGGGTGGATGGTAG	1268
Db	938	ACCTCG	SCCTTGTGTACGCAGCCACATG	TGCTGCTCCAAGCGGTGCGTCTCTTTG	997
QY	1269	CAACTG	AGCTTGTGGCCGGTTTGTGTGT	TGGGATTCGTGTTTACGTTGAGTCA	1328
Db	998	TGAGCC	AGGGTCGTGCGGCCCTCTTCT	CTCGGATGGTCTTTAGCGTCGGCC	1057
QY	1329	AGGAGG	TTT-----ACAATGAATCGA	AGGACTTCGTGAGAGCCAGGTTATTAC	1382
Db	1058	TGGAGG	CTTTGACAAGGACAGCAAGCC	CGATTTTGGAGCTGCAAGTGTCTCTG	1117
QY	1383	GTAACAC	CAAGCGAGGCTGTTTCAACG	ATTGGTTCACTGGGGACTCGACAC	1442
Db	1118	GCAACG	TGACGTGCTCGTCTGGATCG	ACTGGTTTATGGGGCGCCTCAACTAC	1177
QY	1443	AGCATCA	CTGTTTCCAACAATGCC	CAGGCAAACTACCCCAAGATCGCA	1502

Db 1196 CTGGTTCAGGGGACCTCAACTCCAGATCGAGCACCACTCTTCCCCAGGATGCCGAG 1255
QY 1471 GCACAACACTACCCAGATCGCACCTCAGGTCGAGGCTCTTTGCAAGAAGCACGGCCTCGA 1530
Db 1256 ACACAACACTACAGCGGTGCCCCCGCTGGTCAAGTCGTGTGTGCCAAGCACGGCCTCAG 1315
QY 1531 GTACGATAAATGTCCTCGTCGTGGTGCCCTCTGTGCGGTTGTGAAGGCGCTCAAGGAAAT 1590
Db 1316 CTACGAAGTGAAAGCCCTTCCACCGCGCTGTGTGACATCGTCAGGTCCCTGAAGAAGTC 1375
QY 1591 TGCTGA 1596
Db 1376 TGGTGA 1381

RESULT 15
US-08-831-570-1
; Sequence 1, Application US/08831570
; Patent No. 5959175
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Nurborg, Andrew N.
; APPLICANT: Beremand, Phillip D.
; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
; TITLE OF INVENTION: COMPOSITION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; City: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,570
; FILING DATE: 09-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10545
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 743-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
US-08-831-570-1

Query Match 4.3%; Score 87.2; DB 2; Length 1684;
Best Local Similarity 48.4%; Pred. No. 4.9e-15;
Matches 273; Conservative 0; Mismatches 288; Indels 3; Gaps 1;
QY 386 CACGACAGGCCTGGAGACTGCTGGATGATCCTCAAGAGAGAGGTGTATGATATTAGCCGT 445
Db 91 CACGATAAACCCGGAGATCTATGATCTCGATTCAAGGGAAGCCTATGATGTTCCGAT 150
QY 446 TTTGCGGACGACCAACCCCTGGAGGACGGT---AATTAGCACTACTTTGGCGGGATGGC 502
Db 151 TGGGTGAAGAACCATCCAGGTGGCAGCTTTCCCTTGAAGAGATCTTGTGCTCAAGAGGTA 210

QY 503 ACAGACGTTTTTCGCAACATTCATCCACCTGCCGATCGAAGCAACTCAATGACTACTAC 562
Db 211 ACTGATGCAFTTGTTCATTCATCCATCCTGCCTCTACTATGGAAGATCTTGATAAGTTTC 270
QY 563 ATTGGAGACCTTGTAGGGAAGAGCCCTTGTATGATGATGCTTAAAGACTACAGAGATATG 622
Db 271 ACTGGGTATTATCTTAAAGATTACTCTGTCTTCTGAGGTTTCTAAAGATTATAGGAAGCTT 330
QY 623 AGAGCCGAGTTTGTAGAGAAGGGCTTTTCAAGAGTTTCAAGSCCTGGTTCTCTGCTTCAG 682
Db 331 GTGTTGTAGTTTTCTAAATGGGTTTGTATGACAAAAAAGGTCATATTATGTTGCAACT 390
QY 683 ACTCGGATTAATGCAGCTCTCTTCTGCTGCGAGCATTCGACTATCTGTTACGACACAGAT 742
Db 391 TTGTGCTTTATAGCAATGCTGTTTGTCTATGAGTGTATTATGGGTTTGTGTTGAGGGT 450
QY 743 TACTGGGCTATTGTGCTGTCAAGCCAGTTTGTATGGGTCTCTTCCGACAGTGTGGATGG 802
Db 451 GTTTTGGTACATTTGTTTCTGGGTGTTTGAAGGGGTTCTTTGGATTCAGAGTGGTTGG 510
QY 803 CTTGCCCATGATTTCTTCATCAACAGGTCTTTTGAGAACCGTACCGGAACTCCTTCTTT 862
Db 511 ATTGGACATGATGCTGGGCATTATATCGGTAGTGTCTGATTCAAGGCTTAATAAGTTATG 570
QY 863 GGCTATTTGTTCCGAATTCGCTGCTTGGCTTTTAGTATCATGTTGGAGGACGAAGCAC 922
Db 571 GGTATTTTGTGTCAAATTTCTTTTCAGGAATAAGTATTGTTGGTGGAAATGGAACCAT 630
QY 923 AACATTTCATCATACTGCTCCCAAT 946
Db 631 AATGCACATCACATTGCCCTGTAAT 654

Search completed: June 19, 2004, 02:39:11
Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:03:22 ; Search time 59 Seconds
(without alignments)
2313.058 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTDFLNLGLTWSKYSV.....AVVKALKEIADIASIRLHAH 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	2595	100.0	483	4 AAB46436	Aab46436 C. purpur
2	2595	100.0	483	4 AAB46435	Aab46435 C. purpur
3	1619	62.4	520	4 AAB46440	Aab46440 C. purpur
4	1475	56.8	525	3 AAY51354	Aay51354 Protein b
5	1475	56.8	525	4 AAB46810	Aab46810 P. patens
6	1475	56.8	525	5 ABB98277	Abb98277 Physcomit
7	1475	56.8	525	5 ABG73602	Abg73602 P. patens
8	1475	56.8	525	5 ABG73607	Abg73607 P. patens
9	1475	56.8	525	5 ABG73609	Abg73609 P. patens
10	929	35.8	173	4 AAB46437	Aab46437 C. purpur
11	841.5	32.4	457	2 AAW84137	Aaw84137 A delta-6
12	841.5	32.4	457	2 AAW95504	Aaw95504 Mortierel
13	841.5	32.4	457	3 AAY56045	Aay56045 Fungal de
14	841.5	32.4	457	3 AAY92599	Aay92599 M. alpina
15	841.5	32.4	457	4 AAB31684	Aab31684 Amino aci
16	841.5	32.4	458	5 ABG96527	Abg96527 M. alpina
17	841.5	32.4	458	5 ABG96509	Abg96509 M. alpina
18	841.5	32.4	458	5 ABG94707	Abg94707 Human del
19	841.5	32.4	458	5 ABG94693	Abg94693 Human del
20	839.5	32.4	457	2 AAW85121	Aaw85121 A delta-6
21	799.5	30.8	477	5 ABB98275	Abb98275 Phaeodact
22	799.5	30.8	477	5 ABG73600	Abg73600 P. tricolor
23	798.5	30.8	453	6 AAEE31900	Aae31900 Saprolegn
24	790	30.4	459	5 AAEE22063	Aae22063 Pythium i
25	705.5	27.2	467	6 ABB99479	Abb99479 Amino aci

26	663.5	25.6	448	3 AAY71551	Aay71551 Florida b
27	649	25.0	355	2 AAW84139	Aaw84139 Desaturas
28	615	23.7	323	5 ABG96515	Abg96515 M. alpina
29	615	23.7	323	5 ABG94698	Abg94698 Human del
30	611.5	23.6	172	4 AAB46438	Aab46438 C. purpur
31	603.5	23.3	458	3 AAY51348	Aay51348 Sphingoli
32	594	22.9	517	3 AAGC7391	Aagc7391 Arabidops
33	587	22.6	449	3 AAY51334	Aay51334 A. thalia
34	587	22.6	449	3 AAG53861	Aag53861 Arabidops
35	584	22.5	449	3 AAG07392	Aag07392 Arabidops
36	583.5	22.5	422	3 AAY96722	Aay96722 E. gracil
37	583	22.5	449	3 AAY51333	Aay51333 B. napus
38	573	22.1	448	2 AAR98455	Aar98455 Borage de
39	573	22.1	448	2 AAW67471	Aaw67471 Borage de
40	573	22.1	448	2 AAW98130	Aaw98130 Borage de
41	572	22.0	448	6 ABG73417	Abg73417 Borage de
42	570	22.0	448	3 AAY51349	Aay51349 Sunflower
43	568	21.9	449	3 AAG29290	Aag29290 Arabidops
44	567	21.8	448	5 AAU79830	Aau79830 Borage of
45	567	21.8	448	6 ABG73095	Abg73095 Borage de

ALIGNMENTS

RESULT 1
AAB46436
ID AAB46436 standard; protein; 483 AA.
XX
AC AAB46436;
XX
DT 06-APR-2001 (first entry)
XX
DE C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NC 4.
XX
KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic.
XX
OS Ceratodon purpureus.
XX
PN WC200075341-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-EP005274.
XX
PR 07-JUN-1999; 99DE-01025718.
XX
PA 22-DEC-1999; 99DE-01062409.
XX
(BADI) BASF AG.
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX WPI; 2001-112150/12.
XX N-PSDB; AAF25730.
PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
ET producing plant oils with increased content of unsaturated fatty acids.
XX Example 8; Page 49-50; 69pp; German.
CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and 5C; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other

CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (II), e.g. antisense sequences or ribozymes, can
CC be used to suppress expression of (II), resulting in oils with increased
CC content of saturated fatty acids
XX
SQ

Sequence 483 AA;

Query Match 100.0%; Score 2595; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.8e-266;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVTDFLNFLGTTWSKYSVYTHSYAGNYGPTLKHAKKVSAGQKTAGQTLRQSVQDKKP 60
DB 1 MALVTDFLNFLGTTWSKYSVYTHSYAGNYGPTLKHAKKVSAGQKTAGQTLRQSVQDKKP 60
QY 61 GTYSLADVASHDRPGDCWMIKVKYDISRFPADDPGGTIVSTYFGRDGTDFVATFHPPA 120
DB 61 GTYSLADVASHDRPGDCWMIKVKYDISRFPADDPGGTIVSTYFGRDGTDFVATFHPPA 120
QY 121 AWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFVREGFLFKSSKAWFLLQTLINAALFAAS 180
DB 121 AWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFVREGFLFKSSKAWFLLQTLINAALFAAS 180
QY 181 IATICYDKSYWAIIVLSASLMGLFVQCCGWLADHDFLHQQVFENRTANSFEGYLFNCVLGF 240
DB 181 IATICYDKSYWAIIVLSASLMGLFVQCCGWLADHDFLHQQVFENRTANSFEGYLFNCVLGF 240
QY 241 SVSWWRTKXNIHTHTAPNECDEQYTPLEDIDTLPPIAWSKEILATVESKRILRVLYQYHY 300
DB 241 SVSWWRTKXNIHTHTAPNECDEQYTPLEDIDTLPPIAWSKEILATVESKRILRVLYQYHY 300
QY 301 MILPLLEMARYSWTFTGSLLEFTFNPDLSITKGLIEKGTVAFYAWFSAFHLPGVAKPL 360
DB 301 MILPLLEMARYSWTFTGSLLEFTFNPDLSITKGLIEKGTVAFYAWFSAFHLPGVAKPL 360
QY 361 AMWVATELVAGLLLGFTVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWENDWFTGGT 420
DB 361 AMWVATELVAGLLLGFTVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWENDWFTGGT 420
QY 421 QIEHHLFPTMPRHNPYKPIAPQVEALCKKHGLEVDNVSVVGASVAVVKALKEADEASIRL 480
DB 421 QIEHHLFPTMPRHNPYKPIAPQVEALCKKHGLEVDNVSVVGASVAVVKALKEADEASIRL 480
QY 481 HAH 483
DB 481 HAH 483

RESULT 2
AAB46435
ID AAB46435 standard; protein; 483 AA.

AC AAB46435;

XX 06-APR-2001 (first entry)

DE C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 2.

XX Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic.

XX Ceratodon purpureus.

PN WO200075341-A1.

XX 14-DEC-2000.

PF 07-JUN-2000; 2000WO-EP005274.

PR 07-JUN-1999; 99DE-01025718.
PR 22-DEC-1999; 99DE-01062409.

XX (BADI) BASF AG.

XX Heinz E, Szymne S, Lee M, Girke T, Sperling P, Zaehringner U;

XX WPI; 2001-112150/12.

DR N-PSDB; AAF25729.

XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for
PT producing plant oils with increased content of unsaturated fatty acids.

XX Example 8; Page 44-46; 69pp; German.

XX This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (III) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
CC be used to suppress expression of (II), resulting in oils with increased
CC content of saturated fatty acids

XX SQ Sequence 483 AA;

Query Match 100.0%; Score 2595; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.8e-266;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVTDFLNFLGTTWSKYSVYTHSYAGNYGPTLKHAKKVSAGQKTAGQTLRQSVQDKKP 60
DB 1 MALVTDFLNFLGTTWSKYSVYTHSYAGNYGPTLKHAKKVSAGQKTAGQTLRQSVQDKKP 60
QY 61 GTYSLADVASHDRPGDCWMIKVKYDISRFPADDPGGTIVSTYFGRDGTDFVATFHPPA 120
DB 61 GTYSLADVASHDRPGDCWMIKVKYDISRFPADDPGGTIVSTYFGRDGTDFVATFHPPA 120
QY 121 AWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFVREGFLFKSSKAWFLLQTLINAALFAAS 180
DB 121 AWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFVREGFLFKSSKAWFLLQTLINAALFAAS 180
QY 181 IATICYDKSYWAIIVLSASLMGLFVQCCGWLADHDFLHQQVFENRTANSFEGYLFNCVLGF 240
DB 181 IATICYDKSYWAIIVLSASLMGLFVQCCGWLADHDFLHQQVFENRTANSFEGYLFNCVLGF 240
QY 241 SVSWWRTKXNIHTHTAPNECDEQYTPLEDIDTLPPIAWSKEILATVESKRILRVLYQYHY 300
DB 241 SVSWWRTKXNIHTHTAPNECDEQYTPLEDIDTLPPIAWSKEILATVESKRILRVLYQYHY 300
QY 301 MILPLLEMARYSWTFTGSLLEFTFNPDLSITKGLIEKGTVAFYAWFSAFHLPGVAKPL 360
DB 301 MILPLLEMARYSWTFTGSLLEFTFNPDLSITKGLIEKGTVAFYAWFSAFHLPGVAKPL 360
QY 361 AMWVATELVAGLLLGFTVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWENDWFTGGT 420
DB 361 AMWVATELVAGLLLGFTVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWENDWFTGGT 420
QY 421 QIEHHLFPTMPRHNPYKPIAPQVEALCKKHGLEVDNVSVVGASVAVVKALKEADEASIRL 480
DB 421 QIEHHLFPTMPRHNPYKPIAPQVEALCKKHGLEVDNVSVVGASVAVVKALKEADEASIRL 480
QY 481 HAH 483

CC -8-unsaturated long-chain base cis/trans ratio, especially to compensate
CC for a delta-8-unsaturated long-chain base deficiency, to exclude
CC production of delta-8-unsaturated bases, to increase tolerance or
CC resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a protein which has delta6 fatty acid
CC desaturase activity which is described in the method of the invention
XX
SQ Sequence 525 AA;

Query Match 56.8%; Score 1475; DB 3; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-147;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

Qy 1 MALVTDFLNLGTT---WSKYSVYTHSYAGNYGPTLKHAKKVS----- 40
Db 25 MSLFSDFFSVSSSTVGWSVHSIQPLK-----RLTSKKRVSESAAVQCISAEVQRNSS 77
Qy 41 -----AQQKTAGQTLRQRSVQDKKPGTYSIADVASHDRPGDCWMIVKEKYVDIRFADD 94
Db 78 TQGTAEALAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKYVDVSNFADE 136
Qy 95 HPGGTWISTYFGRDGTDFVATFHPAAWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFV 154
Db 137 HPGGSVISTYFGRDGTDFVSSFHAASTWKILQDFYIGDVERVEPTPELLKDFREMRALFL 196
Qy 155 REGLFKSSKAWELLQTLINAALFAASIAIICYSKYSWRTKHNHHTAPNECDEQYTPLEDIDTLP 214
Db 197 REQLFKSSKLYVVMKLLTNVAIFAASIAIICWSKTISAVLASACVMALCFQCGWLSHDF 256
Qy 215 LHQOVFEENTRANSFFGYLFGNCVLGFSVSWRTKHNHHTAPNECDEQYTPLEDIDTLP 274
Db 257 LHNQVFETRWLNEVGVYIGNAVLGFSTGWKEKHNHHAAPNECDQTYQPIDEDIDTLP 316
Qy 275 IIAWSKEILATVESKRILRVLYQHYMILPLLPMARYSWTEGSLLEFTFNPDLSTTKGLIE 334
Db 317 LIAWSKDILATVENKTFRLILQYQHLFFGMGLLFFARGSWLFWWSRYTSTAVLSPVDRLE 376
Qy 335 KGTVAFYHAWFSWAAPHILPGVAKPLAMVATELVAGLLGLGFVFTLSHNGKEVYNESKDF 394
Db 377 KGTVLFHYFWFGVTACYLLPG-WKPLVVMVAVTELMGMLLGFVFLSHNGMEVYNSSKEF 435
Qy 395 VRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMPRHNYPKIAQVVEALCKKHGLEYD 454
Db 496 DVSIATGTCVKLKALKEVA-EAAAEQHA 522

RESULT 5
AAB46810
ID AAB46810 standard; protein; 525 AA.
XX AAB46810;
AC AAB46810;
XX 23-APR-2001 (first entry)
DT
XX P. patens delta6-desaturase protein.
DE Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;
XX fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;
KW agricultural chemical.
KW Physcomitrella patens.
XX
OS
XX WO200102591-A1.
PN
XX

PD 11-JAN-2001.
XX
PF 04-JUL-2000; 2000WO-EP006223.
XX
PR 06-JUL-1999; 99US-00347531.
PR 30-JUN-2000; 2000DE-01030976.
XX
PA (BADI) BASF AG.
XX
PI Heinz E, Girke T, Scheffler J, Da Costa E SilvaO;
XX
DR MPI; 2001-123117/13.
DR N-PSDB; AAF26040.
XX
PT Production of unsaturated fatty acids, useful e.g. in nutrition,
PT cosmetics or pharmaceuticals, in organisms transformed with
PT Physcomitrella patens delta-6-desaturase nucleic acid.
XX
PS Claim 1c; Page 41-43; 49pp; German.
XX
CC This invention describes a novel preparation of unsaturated fatty acids
CC (I) by introducing into an organism at least one isolated nucleic acid
CC (II) that encodes a polypeptide (III) with Delta6-desaturase activity.
CC Organisms that contain at least 1 wt.% (I), on total fatty acid content,
CC are then selected. (II) is selected from: (a) a 2012 bp sequence (S1),
CC defined in the specification, or its equivalents within the degeneracy of
CC the genetic code; or (b) derivatives of the sequence of (a) that encode a
CC 525 amino acid polypeptide (S2), defined in the specification, or a
CC polypeptide with at least 50% homology with (S2) and practically the same
CC enzymatic activity. The invention also describes (1) transgenic organisms
CC that contain (II); and (2) oils, lipids and fatty acids produced by the
CC new method. The oils, lipids and fatty acids produced by the transformed
CC organisms are used in human or animal nutrition, cosmetics,
CC pharmaceuticals and agricultural chemicals. (III) can also be used, in
CC vitro, for increasing the (I) content of triglycerides. The transgenic
CC organisms have increased contents of (I), or of (I)-containing
CC triglycerides, particularly of gamma-linolenic acid
XX
SQ Sequence 525 AA;

Query Match 56.8%; Score 1475; DB 4; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-147;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;
Qy 1 MALVTDFLNLGTT---WSKYSVYTHSYAGNYGPTLKHAKKVS----- 40
Db 25 MSLFSDFFSVSSSTVGWSVHSIQPLK-----RLTSKKRVSESAAVQCISAEVQRNSS 77
Qy 41 -----AQQKTAGQTLRQRSVQDKKPGTYSIADVASHDRPGDCWMIVKEKYVDIRFADD 94
Db 78 TQGTAEALAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKYVDVSNFADE 136
Qy 95 HPGGTWISTYFGRDGTDFVATFHPAAWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFV 154
Db 137 HPGGSVISTYFGRDGTDFVSSFHAASTWKILQDFYIGDVERVEPTPELLKDFREMRALFL 196
Qy 155 REGLFKSSKAWELLQTLINAALFAASIAIICYSKYSWRTKHNHHTAPNECDEQYTPLEDIDTLP 214
Db 197 REQLFKSSKLYVVMKLLTNVAIFAASIAIICWSKTISAVLASACVMALCFQCGWLSHDF 256
Qy 215 LHQOVFEENTRANSFFGYLFGNCVLGFSVSWRTKHNHHTAPNECDEQYTPLEDIDTLP 274
Db 257 LHNQVFETRWLNEVGVYIGNAVLGFSTGWKEKHNHHAAPNECDQTYQPIDEDIDTLP 316
Qy 275 IIAWSKEILATVESKRILRVLYQHYMILPLLPMARYSWTEGSLLEFTFNPDLSTTKGLIE 334
Db 317 LIAWSKDILATVENKTFRLILQYQHLFFGMGLLFFARGSWLFWWSRYTSTAVLSPVDRLE 376
Qy 335 KGTVAFYHAWFSWAAPHILPGVAKPLAMVATELVAGLLGLGFVFTLSHNGKEVYNESKDF 394
Db 377 KGTVLFHYFWFGVTACYLLPG-WKPLVVMVAVTELMGMLLGFVFLSHNGMEVYNSSKEF 435
Qy 395 VRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMPRHNYPKIAQVVEALCKKHGLEYD 454

Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRQIEHHLFPTMPRHNLNKIAPRVEVFCKKHGLVYE 495
QY 455 NVSVVGASVAVVKALKKEIADIASIRLHA 482
Db 496 DVSIAATGTCVKLKEVA-EAAAEQHA 522

RESULT 6
ABB98277
ID ABB98277 standard; protein; 525 AA.
XX
AC ABB98277;
XX
DT 28-MAR-2003 (first entry)
XX
DE Physcomitrella patens desaturase SEQ ID NO 8.
XX
KW Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
KW enzyme.

XX Physcomitrella patens.
XX DE10102337-A1.
XX 25-JUL-2002.
XX 19-JAN-2001; 2001DE-01002337.
XX 19-JAN-2001; 2001DE-01002337.
XX (BADI) BASF PLANT SCI GMBH.
XX Lerchl J, Renz A, Heinz E, Domerque F, Zaehring U;
XX WPI; 2002-644810/70.
XX N-PSDB; ABV74260.

XX Preparing ester containing polyunsaturated fatty acids, useful e.g. in
XX animal or human nutrition, by transforming organism with desaturase gene
XX from Phaeodactylum tricornutum.
XX Example 5; Page 63-65; 182pp; German.

XX The invention relates to preparing (M1) fatty acid esters (I) with an
XX increased content of polyunsaturated fatty acids (II) with at least two
XX double bonds by introducing into a (I)-producing organism a specific
XX nucleic acid (A). (M1) is useful for preparing ester containing
XX polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
XX produced by (M1) are used in animal and human nutrition, cosmetics and
XX pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
XX the blood and to protect against heart disease. Cells that express (A)
XX are also used to identify (ant)agonists of desaturases, e.g. for
XX modulating the yield and rate of production of particular fine chemicals
XX in microorganisms (claimed). Also (A) and derived proteins can be used as
XX markers of specific genomic regions and in evolutionary/protein
XX structural studies. (M1) is suitable for large scale production (no known
XX bioengineering method can produce (II) on a useful scale). The present
XX sequence is that of a Physcomitrella patens desaturase encoded by a cDNA
XX used as the (A) component of the invention in producing transgenic (I)-
XX producing organisms
SQ Sequence 525 AA;

Query Match 56.8%; Score 1475; DB 5; Length 525;
Best Local Similarity 55.3%; Pred. NO. 4e-147;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

QY 1 MALVTDPLNFGTT---WSKYSVYTHSYAGNYGFTLKHAKKVS----- 40
Db 25 MSLFSDFFSYVSSTVGWSVHSIQPLK-----RLTSKGRVSESAAVQCISAEVQRNSS 77

QY 41 -----AQKTAGQTLRQSRWCKKPGTYSLADVASHDRPGDCWMIKVKYVDISRFADD 94
Db 78 TQGTAEALAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVKKNKYDVSFADF 136
QY 95 HPGGTVISTYFGRDGTDFVATFHPAANKQNDYIIGDLAREEPLDELLKDYRDMRAEFV 154
Db 137 HPGGTVISTYFGRDGTDFVSEFFHAASTWKILQDFYIGDVERVEPTPELLKDFEMRALFL 196
QY 155 REGLPKSSKAWFLLQTLINAAALFAASIATICYDKSYWAIVLVSASLMGLFVQCCGWLHDF 214
Db 197 REQLFKSSKLYVVMKLLTNVAIFAASIAIICWSKTIISAVLASACWMAALCFQCCGWLHDF 256
QY 215 LEQOVFENRTANSFFGYLFGNCVLGFSVSWWRTKXNIHHTAPNECDEQYTPLEDIDTLP 274
Db 257 LHNQVFETRWLNEVGVYIGNAVLGFSTGWWKEKHNLHHAAPNECDQTYQPIDEDIDTLP 316
QY 275 ILAWSKEILATVESKRILRVLQYQHMYMILPLLFMARYSWTFGSLLEFTFNPDLSTTKGLIE 334
Db 317 LLAWSKDILATVENKTFLRILQYQHLLFFMGLLFFARGSWLFWRYTSTAVLSPVDRLL 376
QY 335 KGTVAHYAWFSAAFHILPGVAKPLAMWVATELVAGLLGFVFTLSHNGKEVYNESKOF 394
Db 377 KGTVLFHYFWFVGTCYLLPG-WKPLVWMAVTELMGMLGFVFLSHNGMEVYNSKEF 435
QY 395 VRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMPRHNYPKIAPQVEALCKKHGLEVD 454
Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRQIEHHLFPTMPRHNLNKIAPRVEVFCKKHGLVYE 495
QY 455 NVSVVGASVAVVKALKKEIADIASIRLHA 482
Db 496 DVSIAATGTCVKLKEVA-EAAAEQHA 522

RESULT 7

ABG73602
ID ABG73602 standard; protein; 525 AA.

XX
AC ABG73602;
XX
DT 25-MAR-2003 (first entry)
XX
DE P. patens D6 desaturase SEQ ID 8.
XX

KW Promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific.

XX Physcomitrella patens.

XX DE10102338-A1.

XX 25-JUL-2002.

XX 19-JAN-2001; 2001DE-01002338.

XX 19-JAN-2001; 2001DE-01002338.

XX (BADI) BASF PLANT SCI GMBH.

PI Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;

XX WPI; 2002-675961/73.

DR N-PSDB; ABQ76782.

XX
PT New expression cassette for plant genes, useful for preparing transgenic
PT plants that have increased production of polyunsaturated fatty acids.

PS Example 17; Page 67-69; 188pp; German.

XX
CC This invention describes novel expression cassette (EC) containing at
CC least one each of plant promoter (P) and structural gene (SG) expressed
CC in plants, flanked by specific restriction enzyme (RE) recognition sites.

CC The EC has the structure (L1-P-SG-L2)_n where L1 = is a polylinker
CC (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
CC sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
CC sequences and n = 1-3. The invention discloses a vector containing this
CC EC, an organism containing the EC or the vector and a transgenic plant
CC containing a (non-)functional nucleic acid in the vector. Transgenic
CC plants e.g. linseed can be prepared with improved production of fatty acid
CC esters with an increased content of polyunsaturated fatty acids (PUFA),
CC useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
CC PUFA are known to reduce levels of cholesterol in the blood and to
CC protect against heart disease. The expression cassettes of the invention
CC provide increased and more efficient production of fine chemicals
CC (especially PUFA), including seed-specific production. This sequence
CC represents a polynucleotide sequence used to illustrate the method of the
XX invention
SQ Sequence 525 AA;

Query Match 56.8%; Score 1475; DB 5; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-147;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;
QY 1 MALVTDFLNLGTT---WSKYSVYTHSYAGNYGPTLKHKAKVS----- 40
Db 25 MSLFSDFFSYSVSTVGSWSVHSIQPLK-----RLTSKRVSESAAVQCISAEVQRNSS 77
QY 41 -----AQQKTAGQTLRQSRVQDKKPGTYSLADVASHDRPGDCMIVKEKYDISRFAAD 94
Db 78 TQGTAEALAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKYDVSNFADE 136
QY 95 HPGGTIVISTYFGRDGTDFVATFHPPAWQKQNDYYIGDLAREEPLDLKDYRDMRAEFV 154
Db 137 HPGGSVISTYFGRDGTDFVSSFHAASTWKILQDFYIGDVERVEPTPELLKDFREMRALFL 196
QY 155 REGLFKSSKAWFLQLTLINAALFAASTIATICYDKSYWAIVLSASLMGLFVQCGWLAHDF 214
Db 197 REQLFKSSKLYYVMKLLTNVAIFAASIAIICWSKTISAVLASACMMALCFQCGWLSHDF 256
QY 215 LHQOVFENRTANSFFGYLFGNCVLTGFSVSWRTKHNHHHTAPNECDQYTPLEDIDITLP 274
Db 257 LHNQVFETRLNEVGVYIGNAVLGFSTGWWKEKHNHLHHAAPNECDQTYQPIDEDIDTLP 316
QY 275 IIAWSKEILATVESKRILRVLOYQHYMILPLLFMARYSWTFFGSLLETFNPDLSTTKGLIE 334
Db 317 LIAWSKDILATVENKTEFLRILOYQHLEFFMGLFFARGSWLFWWSRYTSTAVLSPVDRILLE 376
QY 335 KGTVAHFYAWFWSWAAAFHILPGVAKPLAWMVATLVAGLLLGFTVTLSHNGKEVYNESKDF 394
Db 377 KGTVLEHYFWFVGTACYLLPG-WKPLVWNAVTELMGMLLGFVFLVSHNGMEVYNSKEF 435
QY 395 VRAQVITFTNTKRGWFNDWFTGGLDTQIEHHLFPTMPRHNYPKIAQVEALCKKHGLEVD 454
Db 436 VSAQIVSTRDKGNIFNDWFTGGLNRQIEHHLFPTMPRHNLNKIAPRVEVFCCKHGLEVYE 495
QY 455 NVSVVGASVAVVKALKKEIADEASIRLHA 482
Db 496 DVSIATGTCVKLKALKEVA-EAAABQHA 522

RESULT 8
ABG73607
ID ABG73607 standard; protein; 525 AA.
XX AC ABG73607;
XX 25-MAR-2003 (first entry)
XX P. patens delta6 desaturase SEQ ID 27.
XX promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific.

XX Physcomitrella patens.
XX DE10102338-A1.
PN 25-JUL-2002.
PD 19-JAN-2001; 2001DE-01002338.
XX 19-JAN-2001; 2001DE-01002338.
PR (BADI) BASF PLANT SCI GMBH.
XX Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
XX WPI; 2002-675961/73.
DR N-PSDB; ABQ76796.
XX New expression cassette for plant genes, useful for preparing transgenic
XX plants that have increased production of polyunsaturated fatty acids.
PT Example 13; Page 155-157; 188pp; German.

CC This invention describes novel expression cassette (EC) containing at
CC least one each of plant promoter (P) and structural gene (SG) expressed
CC in plants, flanked by specific restriction enzyme (RE) recognition sites.
CC The EC has the structure (L1-P-SG-L2)_n where L1 = is a polylinker
CC (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
CC sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
CC sequences and n = 1-3. The invention discloses a vector containing this
CC EC, an organism containing the EC or the vector and a transgenic plant
CC containing a (non-)functional nucleic acid in the vector. Transgenic
CC plants e.g. linseed can be prepared with improved production of fatty acid
CC esters with an increased content of polyunsaturated fatty acids (PUFA),
CC useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
CC PUFA are known to reduce levels of cholesterol in the blood and to
CC protect against heart disease. The expression cassettes of the invention
CC provide increased and more efficient production of fine chemicals
CC (especially PUFA), including seed-specific production. This sequence
CC represents a polynucleotide sequence used to illustrate the method of the
XX invention
SQ Sequence 525 AA;

Query Match 56.8%; Score 1475; DB 5; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-147;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;
QY 1 MALVTDFLNLGTT---WSKYSVYTHSYAGNYGPTLKHKAKVS----- 40
Db 25 MSLFSDFFSYSVSTVGSWSVHSIQPLK-----RLTSKRVSESAAVQCISAEVQRNSS 77
QY 41 -----AQQKTAGQTLRQSRVQDKKPGTYSLADVASHDRPGDCMIVKEKYDISRFAAD 94
Db 78 TQGTAEALAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKYDVSNFADE 136
QY 95 HPGGTIVISTYFGRDGTDFVATFHPPAWQKQNDYYIGDLAREEPLDLKDYRDMRAEFV 154
Db 137 HPGGSVISTYFGRDGTDFVSSFHAASTWKILQDFYIGDVERVEPTPELLKDFREMRALFL 196
QY 155 REGLFKSSKAWFLQLTLINAALFAASTIATICYDKSYWAIVLSASLMGLFVQCGWLAHDF 214
Db 197 REQLFKSSKLYYVMKLLTNVAIFAASIAIICWSKTISAVLASACMMALCFQCGWLSHDF 256
QY 215 LHQOVFENRTANSFFGYLFGNCVLTGFSVSWRTKHNHHHTAPNECDQYTPLEDIDITLP 274
Db 257 LHNQVFETRLNEVGVYIGNAVLGFSTGWWKEKHNHLHHAAPNECDQTYQPIDEDIDTLP 316
QY 275 IIAWSKEILATVESKRILRVLOYQHYMILPLLFMARYSWTFFGSLLETFNPDLSTTKGLIE 334
Db 317 LIAWSKDILATVENKTEFLRILOYQHLEFFMGLFFARGSWLFWWSRYTSTAVLSPVDRILLE 376
QY 335 KGTVAHFYAWFWSWAAAFHILPGVAKPLAWMVATLVAGLLLGFTVTLSHNGKEVYNESKDF 394

Db 377 KGTVLPHYFVFGTACVLLPG-WKPLVWMAVTELMGMLLGFVFLSHNGMEVYNSKEF 435
QY 395 VRAQVITTRNTKRGWFDWFTGGLDTQIEHHLFPTMPRHNYPKIAPQVBALCKKHGLEVD 454
Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRQIEHHLFPTMPRHNLNKIAPRVEVECKKHGLVYE 495
QY 455 NVSVVGASVAVVKALKKEIADEASIRLHA 482
Db 496 DVSIATGTCKVLKALKEVA-EAAAEQHA 522

RESULT 9
ABG73609
ID ABG73609 standard; protein; 525 AA.
XX AC ABG73609;
XX 25-MAR-2003 (first entry)
DE P. patens delta6 desaturase SEQ ID 30.
KW Promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific.
OS Physcomitrella patens.
XX DE10102338-A1.
PN 19-JAN-2001; 2001DE-01002338.
PR 19-JAN-2001; 2001DE-01002338.
XX (BADI) BASF PLANT SCI GMBH.
PI Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
DR WPI; 2002-675961/73.
DR N-PSDB; ABQ76797.
XX New expression cassette for plant genes, useful for preparing transgenic plants that have increased production of polyunsaturated fatty acids.
PS Example 13; Page 176-178; 188pp; German.

CC This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (L1-P-SG-L2) n where L1 = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a (non-)functional nucleic acid in the vector. Transgenic plants e.g linseed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (PUFA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. PUFA are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression cassettes of the invention provide increased and more efficient production of fine chemicals (especially PUFA), including seed-specific production. This sequence represents a polynucleotide sequence used to illustrate the method of the invention

XX Sequence 525 AA;
SQ Query Match 56.8%; Score 1475; DB 5; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-147;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

QY 1 MALVTDLFLNFLTGT--WSKYSVYTHSYAGNYGPTLKHAKKVS----- 40
Db 25 MSLSDFSYSVSSTVGSWSVHSIQPLK-----RLTSKKRVSESAVQCISAEVQRNSS 77
QY 41 -----AQQKTAGQTLRQORSVQDKKPGTYSLADVASHDRPGDCWMIVKEKVDISRADD 94
Db 78 TQGTAEALAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKYDVSNFADE 136
QY 95 HPGGTVIISTYFCGDDTDVFATFHPAAWKQLNDYIIGDIAREEPLDELLKDYRDMZAEFV 154
Db 137 HPGGSVISTYFCGRDGDVFSFHAASTWKILQDFYIGDVERVEPTPELLKDFRMRALFL 196
QY 155 REGLFKSSKAWFLLQTLINAALFAASIATICYDKSYWAIIVLSASLMGLFVQQCGWLHADF 214
Db 197 REQLFKSSKLYYVMKLLTNVAIFAASIAIICWSKTIISAVLASACMMALCFQQCGWLSHDF 256
QY 215 LHQQVFENRTANSFFGYLFGNCVLGFSVSWKPKHNIHHTAPNECDEQYTPLDEIDITLP 274
Db 257 LHNQVFETRNLNEVVGVVIGNAVLGFSTGWNKXKHNHLHHAAPNECDQTYQPIDEDITLP 316
QY 275 IIAWSKEILATVESKRILRVLOYQHYMILPLFPMARYSWTFGSLFTFNPDLSTTKGLIE 334
Db 317 LIAWSKDILATVENKTFLRILQYQHLFFMGLLFPARGSWLFSWRYTSTAVLSPVDRILLE 376
QY 335 KGTVAFHAYWFSWAAPHILPGVAKPLAMWVATELVAGLLGFVFTLSHNGKEVYNESKDF 394
Db 377 KGTVLPHYFVFGTACVLLPG-WKPLVWMAVTELMGMLLGFVFLSHNGMEVYNSKEF 435
QY 395 VRAQVITTRNTKRGWFDWFTGGLDTQIEHHLFPTMPRHNYPKIAPQVBALCKKHGLEVD 454
Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRQIEHHLFPTMPRHNLNKIAPRVEVECKKHGLVYE 495
QY 455 NVSVVGASVAVVKALKKEIADEASIRLHA 482
Db 496 DVSIATGTCKVLKALKEVA-EAAAEQHA 522

RESULT 10
AAB46437
ID AAB46437 standard; protein; 173 AA.
XX AC AAB46437;
XX 06-APR-2001 (first entry)
DT C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 6.
DE Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic.
XX Ceratodon purpureus.
PN WO2000075341-A1.
XX 14-DEC-2000.
PF 07-JUN-2000; 2000WO-EP005274.
XX 07-JUN-1999; 99DE-01025718.
PR 22-DEC-1999; 99DE-01062409.
XX (BADI) BASF AG.
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX WPI; 2001-112150/12.
DR N-PSDB; AAF25731.
XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids.

PS Example 8; Page 51-52; 69pp; German.

XX This invention describes a novel isolated nucleic acid (I) encoding

CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase

CC activity. The invention also describes (a) amino acid sequences encoded

CC by (I); (b) an expression cassette (EC) containing (I) linked to one or

CC more regulatory sequences; (c) a vector containing (I) and EC; (d)

CC organisms containing (I), EC or the vectors of (c); (e) preparation of

CC unsaturated fatty acids (A) or triglycerides (TG) with increased content

CC of (A) by introducing (I) or EC into an oil-producing organism; (f)

CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)

CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by

CC method (g). (I) are used to produce transgenic plants (or other

CC organisms) that produce oils or triglycerides (TG) with increased content

CC of unsaturated fatty acids (A) and to isolate related sequences by

CC homology screening. (A), or TG containing them, are useful in human

CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and

CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can

CC be used to suppress expression of (I), resulting in oils with increased

CC content of saturated fatty acids

XX

SQ Sequence 173 AA;

Query Match 35.3%; Score 929; DB 4; Length 173;

Best Local Similarity 100.0%; Pred. No. 7.1e-90;

Matches 173; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 251 IHHTAPNECDEQYTPLEDEDITPLIAWSKEILATVESKRILRVLOQYHYMILPLEMAR 310

Db 1 IHHTAPNECDEQYTPLEDEDITPLIAWSKEILATVESKRILRVLOQYHYMILPLEMAR 60

Qy 311 YSWTFGSLLETFNPDLSSTTKGLIEKGTVAFHAYAFWSWAAPHILPGVAKPLAWMVATELVA 370

Db 61 YSWTFGSLLETFNPDLSSTTKGLIEKGTVAFHAYAFWSWAAPHILPGVAKPLAWMVATELVA 120

Qy 371 GLLLGFTVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWENDWFTGGLDTQIE 423

Db 121 GLLLGFTVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWENDWFTGGLDTQIE 173

RESULT 11

AAW84137

ID AAW84137 standard; protein; 457 AA.

XX

AC AAW84137;

XX

DT 15-FEB-1999 (first entry)

XX

DE A delta-6 desaturase enzyme.

XX

KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition;

KW inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes;

KW eczema; platelet aggregation; vasodilation; cholesterol level;

KW endometriosis; premenstrual syndrome; myalgic encephalomyelitis;

KW chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome;

KW hypertension; inflammatory skin disorder.

XX

OS Mortierella alpina.

XX

PN WO9846763-A1.

XX

PD 22-OCT-1998.

XX

PF 10-APR-1998; 98WO-US007126.

XX

PR 11-APR-1997; 97US-00834655.

XX

PA (CALJ) CALGENE LLC.

PA (ABBO) ABBOTT LAB.

XX

PI Knutzon D, Mukerji P, Huang Y, Thurmond J, Chaudhary S;

PI Leonard AE;

XX

DR WPI; 1998-594582/50.

DR N-PSDB; AAV63624.

XX

PT New isolated fatty acid desaturase enzymes - used for the production of

PT polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions,

PT nutritional compositions, cosmetics or animal feed.

XX

PS Claim 3; Fig 3A-E; 165pp; English.

XX

CC The present sequence represents a Mortierella alpina fatty acid delta-6

CC desaturase enzyme. The enzyme sequence is used in the methods of the

CC invention. The specification describes methods for desaturating a fatty

CC acid and for producing a desaturated fatty acid by expressing increased

CC levels of a desaturase. The present desaturase is an enzyme which

CC introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty

CC acid molecule. The enzyme can be used for desaturating fatty acids. The

CC enzyme can be used to produce polyunsaturated fatty acids, which can be

CC used for treating malnutrition, in pharmaceutical compositions, in

CC cosmetics or in animal feed. The polyunsaturated fatty acids can be used

CC for treating e.g. restenosis after angioplasty, inflammation, rheumatoid

CC arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood

CC pressure. They can also be used to inhibit platelet aggregation, cause

CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel

CC wall smooth muscle and fibrous tissue, reduce or prevent gastro-

CC intestinal bleeding and other side effects caused by non-steroidal anti-

CC inflammatory drugs, prevent or treat endometriosis and premenstrual

CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral

CC infections, treat AIDS, multiple sclerosis, acute respiratory syndrome,

CC hypertension and inflammatory skin disorders

XX

SQ Sequence 457 AA;

Query Match 32.4%; Score 841.5; DB 2; Length 457;

Best Local Similarity 39.2%; Pred. No. 6.3e-80;

Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

Qy 62 TVSLADV-----ASHDRPGDCWMIVKEKVDISRFADHPGCTVISTYFGRDGTDVF 113

Db 9 TFRAEVLNAEALNEGKDAEAPFLMIIDNKVYDVRFEVDHPGGSVILTHVGKDGTDVF 68

Qy 114 ATFHPPAAWKQNDYVIGDL---AREEPLDELLKDYDRMRAEFVREGLFKSSKAWFLLO 170

Db 69 DTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRLKLTFLQSLGYDSSKAYYAFKV 128

Qy 171 LINAALFAASIATICY--DKSYWAIVLASLMGLFVQCQGLAHDFLHQOVFENRTANSF 228

Db 129 SENLCIWGLSTVIVAKWGQSTLANVLSAALLGLFWQCQGLAHDFLHQVQDRFWGDL 188

Qy 229 FGYLEFGNCVLGFSVSWWRTKXNHHTAPNECDEQYTPLEDEDITPLIAWSK---EILAT 285

Db 189 FGAFLLGGVCQGFSSSWWKKDXTNTHAAPNVHGE-----DPDIDTHPLLTWSEHALEMFS 243

Qy 286 VESKRILRVLOQYHYMIL-----PLLFMARYSWTFGSLLETFNPDLSSTTK----- 330

Db 244 VPDEBELTRM--WSRFMVLNQTFWYFPILSFARLSWCLOSILFVL-PNGQAHKPSGARVPI 300

Qy 331 GLIEKGTVAFHAYAFWSWAAPHILPGVAKPLAWMVATELVAGLLGFVFTLSHNGKEVYNE 390

Db 301 SLVEQLSLAMHTWYLATMFLFIKDPVNMVLVFLVSQAVCGMLLAIVFSLNHNMGMPVISK 360

Qy 391 SK---DFVRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMPRHNYPKIAPQVEALC 446

Db 361 EEAVDMDFETKQIITGRDVHPGLFANWFTGGLNYQYIEHHLFPPMPRHNFSKIQPAVETLC 420

Qy 447 KKHGLEVDNVSVVGASVAVVAKLKEIADEAS 477

Db 421 KKYNVRYHTTGMIERGTAEVFSRLNEVSKAAS 451

RESULT 12

AAW95504

ID AAW95504 standard; peptide; 457 AA.

XX

Db 301 SLVEQLSLAMHTWYLATMFLFKDPVNMLVFLVSQAVCGNLLAIVFSLNHNGMPWISK 360
QY 391 SK---DEVRAQVITTRNTKRGWENDWFTGGDLTQIEHHLFPTMPRHNYPKIAQVEALC 446
Db 361 EEAVDMDFFTKQIITGRDVHPGLFANWFTGSLNYQIEHHLFSPMRHNFSKIQPAVETLC 420
QY 447 KKHGLEVDNVSVGASVAVVKALKEIADNAS 477
Db 421 KKNVRYHTTGMIEGTAEVFSRLNEVSKAAS 451

RESULT 15
AAB31684
ID AAB31684 standard; protein; 457 AA.
XX
AC AAB31684;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a fungal delta6 desaturase.
XX
KW delta6 desaturase; desaturase gene; elongase gene; fatty acid;
KW eicosanoid; nutrition; infant formula; dietary supplement;
KW dietary substitute; animal feed.
XX

OS Mortierella alpina.
XX
XX WO200104636-A1.
PN
XX 18-JAN-2001.
PD
XX 11-JUL-2000; 2000WO-US019011.
PF
XX 12-JUL-1999; 99US-00351525.
PR
XX (UYOH-) UNIV OHIO.
PA
XX Kopchick JJ, Kelder B;
PI
XX WPI; 2001-182622/18.
DR
DR N-PSDB; AAF25234.
XX

New compositions comprising cells that express desaturases and elongases, for synthesizing essential fatty acids or long-chain polyunsaturated fatty acids, used in nutritional, cosmetic or animal feed formulations.
XX
PS Disclosure; Fig 9; 93pp; English.
XX

The present sequence represents a delta6 desaturase. The desaturase polynucleotide sequence was used to transfect mammalian cells, to produce animal cells expressing a desaturase gene and/or an elongase gene. Compositions comprising cells of the invention are useful for synthesizing essential fatty acids, their derivatives or downstream products, as well as altered levels of long-chain polyunsaturated fatty acids and eicosanoids. The compositions are useful in nutritional formulae, e.g. infant formula, dietary supplements or dietary substitutes for both humans and animals. The compositions are also useful in cosmetic or animal feed formulations. Furthermore, the compositions may also be used as fat free media or as research reagents
XX
SQ Sequence 457 AA;

Query Match 32.4%; Score 841.5; DB 4; Length 457;
Best Local Similarity 39.2%; Pred. No. 6.3e-80;
Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

QY 62 TYSLADV-----ASHDRPGDCWMIIVKEKVDISRFDADHPGGTIVSTYFGRDGTDF 113
Db 9 TETRAEVLNAAENEGKKDAEAPFLMIIDNKVDVREFVPDHPGGSVILTHVGKDGTDVF 68
QY 114 ATFHPPAAWKQINDYYIGDL---AREEPLDELLKDYRDMRAEFVREGFKSSKAWFLLQT 170
Db 69 LTFHPEAAWETLANFYVGDI DESDRDIKNDPFAAEVRKLRTLFQSLGYDSSKAYYAFKV 128

QY 171 LINAALFAASIATICY--DKSYWAIIVLSASLMGLFVQCCGWLADHFLHQQVFENRTANSF 228
Db 129 SFNLCTWSELSTVIVAKWGQSTSLANVLSAALLGLFWQCCGWLADHFLHQQVFQDRFWGDL 188
QY 229 FGYLEFNCVLGFSVSWRTKHNHHTAPNECDEQYTPLEDIDITLPIIAWSK---EILAT 285
Db 189 FGAFLGVCQCGFSSWWKDKHNTTHAAPNVEGE-----DPDIDITHPLLTWSEHALEMFS 243
QY 286 VESKRILRVLYQYQHMYL-----PLLFMARYSWTFGSLLFTEFNPDLSTTK----- 330
Db 244 VPDEELTRM--WSRFMVNLQNTWTFYFPILSPARLSWCLQSILFVL-PNGQAHKPSGARVPI 300
QY 331 GLIEKGTVAFHAYAFSWAAAFHILPGVAKPLAMVAVATELVAGLLLGFFVFTLSHNGKEVYNE 390
Db 301 SLVEQLSLAMHTWYLATMFLFKDPVNMLVFLVSQAVCGNLLAIVFSLNHNGMPWISK 360
QY 391 SK---DEVRAQVITTRNTKRGWENDWFTGGDLTQIEHHLFPTMPRHNYPKIAQVEALC 446
Db 361 EEAVDMDFFTKQIITGRDVHPGLFANWFTGSLNYQIEHHLFSPMRHNFSKIQPAVETLC 420
QY 447 KKHGLEVDNVSVGASVAVVKALKEIADNAS 477
Db 421 KKNVRYHTTGMIEGTAEVFSRLNEVSKAAS 451

Search completed: June 16, 2004, 19:08:06
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:05:56 ; Search time 49 Seconds
(without alignments)
2777.015 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTDFLNFGLTWSKYSV.....AVVKALKEIADEASIRLHAH 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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17:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1475	56.8	525	12	US-10-250-821-8
2	1475	56.8	525	12	US-10-250-821-27
3	1475	56.8	525	12	US-10-250-821-30
4	1475	56.8	525	12	US-10-250-553-8
5	1475	56.8	525	12	US-10-250-553-27
6	1475	56.8	525	12	US-10-250-553-30
7	841.5	32.4	457	14	US-10-278-391-4
8	841.5	32.4	458	14	US-10-191-513A-12
9	841.5	32.4	458	14	US-10-191-513A-41
10	799.5	30.8	477	12	US-10-250-921-4
11	799.5	30.8	477	12	US-10-250-553-4
12	798.5	30.8	453	10	US-C9-769-863-14
13	798.5	30.8	453	14	US-10-054-534B-14
14	798.5	30.8	453	14	US-10-431-952-14
15	790	30.4	459	9	US-09-967-477B-8

16	615	23.7	323	14	US-10-191-513A-17	Sequence 17, Appl
17	603.5	23.3	458	14	US-10-340-779A-11	Sequence 11, Appl
18	587	22.6	448	12	US-10-424-599-199828	Sequence 199828,
19	587	22.6	453	12	US-10-425-114-48669	Sequence 48669, A
20	574	22.1	448	14	US-10-340-779A-13	Sequence 13, Appl
21	567	21.8	443	14	US-10-340-779A-20	Sequence 20, Appl
22	567	21.8	448	13	US-10-029-756-5	Sequence 5, Appli
23	567	21.8	448	16	US-10-702-777-5	Sequence 5, Appli
24	549	21.2	444	12	US-10-231-956A-69	Sequence 69, Appl
25	549	21.2	444	16	US-10-429-160-22	Sequence 22, Appl
26	549	21.2	473	16	US-10-415-232-4	Sequence 4, Appli
27	547	21.1	444	14	US-10-262-617-3	Sequence 3, Appli
28	546	21.0	444	14	US-10-191-513A-12	Sequence 12, Appl
29	546	21.0	515	16	US-10-389-566-447	Sequence 447, App
30	542	20.9	451	12	US-10-424-599-179631	Sequence 179631,
31	542	20.9	497	12	US-10-425-114-52563	Sequence 52563, A
32	539	20.8	425	12	US-10-296-115-1240	Sequence 1240, Ap
33	535	20.6	473	15	US-10-369-493-6108	Sequence 6108, Ap
34	534.5	20.6	444	14	US-10-191-513A-42	Sequence 42, Appl
35	532.5	20.5	432	14	US-10-191-513A-9	Sequence 9, Appli
36	532.5	20.5	465	14	US-10-191-513A-38	Sequence 38, Appl
37	528	20.3	444	12	US-10-239-652A-7	Sequence 7, Appli
38	528	20.3	444	16	US-10-429-160-26	Sequence 26, Appl
39	528	20.3	473	12	US-10-239-652A-8	Sequence 8, Appli
40	526.5	20.3	447	16	US-10-415-232-3	Sequence 3, Appli
41	521	20.1	452	13	US-10-029-756-27	Sequence 27, Appl
42	521	20.1	452	16	US-10-702-777-27	Sequence 27, Appl
43	514	19.8	445	14	US-10-262-617-1	Sequence 1, Appli
44	514	19.8	490	12	US-10-296-115-1301	Sequence 1301, Ap
45	511	19.7	473	12	US-10-239-652A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-250-821-8
; Sequence 8, Application US/10250821
; Publication No. US20040049805A1
; GENERAL INFORMATION:
; APLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Method for the Expression of Biosynthetic Genes
; TITLE OF INVENTION: in Plant Seeds Using Multiple Expression Constructs
; FILE REFERENCE: 2000-904
; CURRENT APPLICATION NUMBER: US/10/250,821
; CURRENT FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 8
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-10-250-821-8

Query Match 56.8%; Score 1475; DB 12; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-146;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

QY	1	MALVTDFLNFGLT---	WSKYSVYTHSYAGNYGPTLKHKVVS-----	40
DB	25	MSLFSDFFSYSSVTGWSVHSIQPLK-----	RLTSKRVSESAAVQCISAEVQRNSS	77
QY	41	-----AQQKTAGQTLRQSVQDKPGTYSLADVASHDRPGDCWMI	VKEKVDISREADD	94
DB	78	TQGTAEALAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCW	IVVKNKYDVSNFADE	136
QY	95	HPGGTVISTYFGRDGTDFEATFHPAAWKQNDYIGDLAREEP	LDLLKDYRDMRAEFV	154
DB	137	HPGGSVISTYFGRDGTDFVFSFHAASTWKILQDFYIGDVER	VEPTPELLKDFREMLLEL	196
QY	155	REGLFKSSKAWFLLOTLINAALFAASIATICYDKSYWAI	VLASLMGLFVQCCGWLHDF	214
DB	197	REQLFKSSKLYYVMKLLTNVAIFAASIAIICWSKTISAV	LASACMMALCFQCCGWLSHDF	256

QY 215 LHQQVFENRTANSFFGYLFGNCVLGFSVSWWRTKHNHHTAPNECDEQYTPLEDIDITLP 274
Db 257 LHNQVFETRLNEVGVYVGNVAVLPG-WKPLVWMAVTELMGMLLGFVFLSHNGMEVYNSKEF 316
QY 275 IIAWSKEILATVESKRILRLVLYQHYMILPLLFMRYSWTFGSLFTFPDLSSTKGLIE 334
Db 317 LIAWSKOILATVENKTFLRILQYQHLFFMGLLFFARGSWLFWWSRYTSTAVLSPVDRLE 376
QY 335 KGTVAHFYAWFSAAPHILPGVAKPLAMVATELVAGLLLGFTLTLSHNGKEVYNSKDF 394
Db 377 KGTVLFFHYFWFVGTACYLLPG-WKPLVWMAVTELMGMLLGFVFLSHNGMEVYNSKEF 435
QY 395 VRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMRHNYPKIAPQVEALCKKHGLEVD 454
Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRQIEHHLFPTMRHNLNKIAPRVEVFCKKHGLEVYE 495
QY 455 NVSVVGASVAVVKALKEIADEASIRLHA 482
Db 496 DVSIATGTCKVLKALKEVA-EAAAEQHA 522

RESULT 2
US-10-250-821-27
; Sequence 27, Application US/10250821
; Publication No. US20040049805A1
; GENERAL INFORMATION:
; APPLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Method for the Expression of Biosynthetic Genes
; FILE REFERENCE: 2000-904
; CURRENT APPLICATION NUMBER: US/10/250,821
; CURRENT FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 27
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: pflanz. Expressionsvektor mit zwei Promotor-
; OTHER INFORMATION: Terminator-Expressionskassetten inseriert ist
; OTHER INFORMATION: Physcomitrella patens Elongase und Desaturase
US-10-250-821-27

Query Match 56.8%; Score 1475; DB 12; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-146;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;
QY 1 MALVTDFLNFELGTT---WSKYSVYTHSVAGNYGPTLKHKAKVS----- 40
Db 25 MSLFSDFFSYVSSVTGWSVSHSIQPLK-----RLTSKRVSESAAVQCISAEVQRNSS 77
QY 41 -----AQQKTAGQTLRQSVQDKPGTYSLADVASHDRPGDCWMIYKEKYDISRFADD 94
Db 78 TQGTAEALAEVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKVDVSNFADE 136
QY 95 HPGGTVISYFGRDGTDFEATFHPAAWKQLNDYIYIGDLAREEPLDELLKDYRDMRAEFV 154
Db 137 HPGGSVISYFGRDGTDFVSSFHAASWTKILQDFYIGDVERVEPTPELLKDFREMRLFL 196
QY 155 REGLEKSSKAWFLQLTLINAALFAASIAIICWSKTISAVLASACMMALCFQCCGWLASHDF 214
Db 197 REQLFKSSKLYYVMKLLTNVAIFAASIAIICWSKTISAVLASACMMALCFQCCGWLASHDF 256
QY 215 LHQQVFENRTANSFFGYLFGNCVLGFSVSWWRTKHNHHTAPNECDEQYTPLEDIDITLP 274
Db 257 LHNQVFETRLNEVGVYVGNVAVLPG-WKPLVWMAVTELMGMLLGFVFLSHNGMEVYNSKEF 316
QY 275 IIAWSKEILATVESKRILRLVLYQHYMILPLLFMRYSWTFGSLFTFPDLSSTKGLIE 334
Db 317 LIAWSKOILATVENKTFLRILQYQHLFFMGLLFFARGSWLFWWSRYTSTAVLSPVDRLE 376
QY 395 VRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMRHNYPKIAPQVEALCKKHGLEVD 454
Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRQIEHHLFPTMRHNLNKIAPRVEVFCKKHGLEVYE 495

QY 335 KGTVAHFYAWFSAAPHILPGVAKPLAMVATELVAGLLLGFTLTLSHNGKEVYNSKDF 394
Db 377 KGTVLFFHYFWFVGTACYLLPG-WKPLVWMAVTELMGMLLGFVFLSHNGMEVYNSKEF 435
QY 395 VRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMRHNYPKIAPQVEALCKKHGLEVD 454
Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRQIEHHLFPTMRHNLNKIAPRVEVFCKKHGLEVYE 495
QY 455 NVSVVGASVAVVKALKEIADEASIRLHA 482
Db 496 DVSIATGTCKVLKALKEVA-EAAAEQHA 522
RESULT 3
US-10-250-821-30
; Sequence 30, Application US/10250821
; Publication No. US20040049805A1
; GENERAL INFORMATION:
; APPLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Method for the Expression of Biosynthetic Genes
; FILE REFERENCE: 2000-904
; CURRENT APPLICATION NUMBER: US/10/250,821
; CURRENT FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 30
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: pflanz. Expressionsvektor mit 3
; OTHER INFORMATION: Promotor-Terminator- Expressionskassetten
; OTHER INFORMATION: inseriert mit Physcomitrella Elongase + Desaturase
; OTHER INFORMATION: + Phaeodactylum Desaturase
US-10-250-821-30

Query Match 56.8%; Score 1475; DB 12; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-146;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;
QY 1 MALVTDFLNFELGTT---WSKYSVYTHSVAGNYGPTLKHKAKVS----- 40
Db 25 MSLFSDFFSYVSSVTGWSVSHSIQPLK-----RLTSKRVSESAAVQCISAEVQRNSS 77
QY 41 -----AQQKTAGQTLRQSVQDKPGTYSLADVASHDRPGDCWMIYKEKYDISRFADD 94
Db 78 TQGTAEALAEVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKVDVSNFADE 136
QY 95 HPGGTVISYFGRDGTDFEATFHPAAWKQLNDYIYIGDLAREEPLDELLKDYRDMRAEFV 154
Db 137 HPGGSVISYFGRDGTDFVSSFHAASWTKILQDFYIGDVERVEPTPELLKDFREMRLFL 196
QY 155 REGLEKSSKAWFLQLTLINAALFAASIAIICWSKTISAVLASACMMALCFQCCGWLASHDF 214
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QY 215 LHQQVFENRTANSFFGYLFGNCVLGFSVSWWRTKHNHHTAPNECDEQYTPLEDIDITLP 274
Db 257 LHNQVFETRLNEVGVYVGNVAVLPG-WKPLVWMAVTELMGMLLGFVFLSHNGMEVYNSKEF 316
QY 275 IIAWSKEILATVESKRILRLVLYQHYMILPLLFMRYSWTFGSLFTFPDLSSTKGLIE 334
Db 317 LIAWSKOILATVENKTFLRILQYQHLFFMGLLFFARGSWLFWWSRYTSTAVLSPVDRLE 376
QY 335 KGTVAHFYAWFSAAPHILPGVAKPLAMVATELVAGLLLGFTLTLSHNGKEVYNSKDF 394
Db 377 KGTVLFFHYFWFVGTACYLLPG-WKPLVWMAVTELMGMLLGFVFLSHNGMEVYNSKEF 435
QY 395 VRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMRHNYPKIAPQVEALCKKHGLEVD 454
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; TITLE OF INVENTION: biosynthesis genes, and novel plant expression
; FILE REFERENCE: 2000-873
; CURRENT APPLICATION NUMBER: US/10/250,553
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 27
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Plant expression vector with two promoter-
; OTHER INFORMATION: terminator expression cassettes;
; OTHER INFORMATION: Physcomitrella patens elongase and desaturase are inserted
US-10-250-553-27

Query Match          56.8%; Score 1475; DB 12; Length 525;
Best Local Similarity 55.3%; Pred. No. 4e-146;
Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

QY 1 MALVTDLFLNPLGTT---WSKYSVYTHSYAGNYGPTLKHKAKVS----- 40
Db 25 MSLFSDFFSYVSTVGSWSVHSIQPLK-----RLTSKRVSESAAVQCISAEVQRNSS 77

QY 41 -----AQKTAGQTLRQSVQDKKPGTYSLADVASHDRPGDCWMIVKEKVVYDISRFADD 94
Db 78 TQGTAEALAESVVKPTRRRSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKVVYDVSNFADE 136

QY 95 HPGGTVISTYFGRDGTDFVATFHPHPPAAWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFV 154
Db 137 HPGGSVISTYFGRDGTDFVFSFHAASTWKILQDFYIGDVERVEPTPELLKDFRMRALFL 196

QY 155 REGLFKSSKAWFLLQTLINAAALFAASIAIICWSKTISAVLASACMMALCFQCCGWLSHDF 214
Db 197 REQLFKSSKLYYVMKLLTNVAIFAASIAIICWSKTISAVLASACMMALCFQCCGWLSHDF 256

QY 215 LHQQVFENRTANSFFGYLFGNCVLGFSVSWRTKHNHHTAPNECDEQYTPLDEDIDTLP 274
Db 257 LHQVFEFTRWLNVEVGVYIGNAVLGFSTGWWKEKHNHLHHAAPNECDQTYQPIDEDIDTLP 316

QY 275 ILAWSKEILATVESKRILRVLYQHYMILPLLFMARYSWTFGSLFTFNPDLSTTKGLIE 334
Db 317 LIAWSKDILATVENKTFLRLQYQHLFFFMGLLFFARGSWLFWWSRYTSTAVLSPVDRLL 376

QY 335 KGTVAFYAWFSWAFAFHILPGVAKPLAWMVATELVAGLLGFVFTLSHNGKEVYNESKDF 394
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Db 496 DVSIATGTCVKLKEVA-EAAAEQHA 522

RESULT 6
US-10-250-553-30
; GENERAL INFORMATION:
; APPLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Production of polyunsaturated fatty acids, novel
; TITLE OF INVENTION: biosynthesis genes, and novel plant expression
; TITLE OF INVENTION: constructs
; FILE REFERENCE: 2000-873
; CURRENT APPLICATION NUMBER: US/10/250,553
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Vers. 2.0
; OTHER INFORMATION: + Phaeodactylum desaturase inserted
US-10-250-553-30

; TITLE OF INVENTION: biosynthesis genes, and novel plant expression
; FILE REFERENCE: 2000-873
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; NUMBER OF SEQ ID NOS: 31
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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Vers. 2.0
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US-10-250-553-30

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US-10-250-553-30

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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Vers. 2.0
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US-10-250-553-30

; TITLE OF INVENTION: biosynthesis genes, and novel
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; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Thraustochytrium sp.
JS-09-967-477B-8

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Job time : 51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: June 18, 2004, 22:56:20 ; Search time 592 Seconds
(without alignments)
3466.013 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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8: Geneseqn2003bs:
9: Geneseqn2003cs:
10: Geneseqn2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2595	100.0	2040	AAF25729	Aaf25729 C. purpur
3	1619	62.4	2160	AAF25734	Aaf25734 C. purpur
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5	1475	56.8	1578	ABQ76782	Abq76782 P. patens
6	1475	56.8	2012	AAF26040	Aaf26040 P. patens
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9	1475	56.8	15430	6	ABQ76796	Abq76796 pB-DHGLA
10	1475	56.8	17752	6	ABV74275	Abv74275 Plant spe
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12	925	35.6	520	4	AAF25731	Aaf25731 C. purpur
13	841.5	32.4	1374	3	AAZ47129	Aaz47129 Fungal de
14	841.5	32.4	1374	5	AAF25234	Aaf25234 Nucleotid
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16	841.5	32.4	1617	2	AAX00889	Aax00889 Mortierel
17	841.5	32.4	1617	3	AAA09430	Aaa09430 M. alpina
18	799.5	30.8	1434	6	ABV74258	Abv74258 Phaeodact
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22	705.5	27.2	1404	7	ABV76916	Abv76916 Nucleotid
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ALIGNMENTS

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DT 06-APR-2001 (first entry)
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KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic; ds.
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OS Ceratodon purpureus.
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FH Key Location/Qualifiers
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FT /*tag= a
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Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
WPI; 2001-112150/12.
P-PSDB; AAB46436.

Nucleic acid encoding delta6-acetylenase or desaturase, useful for
producing plant oils with increased content of unsaturated fatty acids.

Claim 1a; Page 46-48; 69pp; German.

This invention describes a novel isolated nucleic acid (I) encoding
polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
activity. The invention also describes (a) amino acid sequences encoded
by (I); (b) an expression cassette (EC) containing (I) linked to one or
more regulatory sequences; (c) a vector containing (I) and EC; (d)
organisms containing (I), EC or the vectors of (c); (e) preparation of
unsaturated fatty acids (A) or triglycerides (TG) with increased content
of (A) by introducing (I) or EC into an oil-producing organism; (f)
proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
production of (A) or TG by using (Ia); and (h) (A) and TG produced by
method (g). (I) are used to produce transgenic plants (or other
organisms) that produce oils or triglycerides (TG) with increased content
of unsaturated fatty acids (A) and to isolate related sequences by
homology screening. (A), or TG containing them, are useful in human
nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
be used to suppress expression of (II), resulting in oils with increased
content of saturated fatty acids

Sequence 1467 BP; 356 A; 349 C; 379 G; 383 T; 0 U; 0 Other;

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Score:	2595.00
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Best Local Similarity:	100.00%
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DB:	4
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Matches:	483
Conservative:	0
Mismatch:	0
Indels:	0
Gaps:	0

JS-09-980-468-2 (1-483) x AAF25730 (1-1467)

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XX 06-APR-2001 (first entry)
XX C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 1.
XX Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic; ds.
XX Ceratodon purpureus.
OS
XX
FH Location/Qualifiers
FT 176..1627
FT /*tag= a
FT /product= "delta6-acetylenase/delta6-desaturase"
XX
PN WO200075341-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-EP005274.
XX
PR 07-JUN-1999; 99DE-01025718.
PR 22-DEC-1999; 99DE-01062409.
XX
PA (BADI) BASF AG.
XX
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring U;
XX
XX MPI; 2001-112150/i2.
DR P-PSDB; AAB46435.
XX

XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for
PT producing plant oils with increased content of unsaturated fatty acids.
XX

ES Claim 1a; Page 41-44; 69pp; German.

XX This invention describes a novel isolated nucleic acid (I) encoding
XX polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
XX activity. The invention also describes (a) amino acid sequences encoded
XX by (I); (b) an expression cassette (BC) containing (I) linked to one or
XX more regulatory sequences; (c) a vector containing (I) and EC; (d)
XX organisms containing (I), EC or the vectors of (c); (e) preparation of
XX unsaturated fatty acids (A) or triglycerides (TG) with increased content
XX of (A) by introducing (I) or EC into an oil-producing organism; (f)
XX proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
XX production of (A) or TG by using (Ia); and (h) (A) and TG produced by
XX method (g). (I) are used to produce transgenic plants (or other
XX organisms) that produce oils or triglycerides (TG) with increased content
XX of unsaturated fatty acids (A) and to isolate related sequences by
XX homology screening. (A), or TG containing them, are useful in human
XX nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
XX cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
XX be used to suppress expression of (II), resulting in oils with increased
XX content of saturated fatty acids

SQ Sequence 2040 BP; 528 A; 450 C; 505 G; 557 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.62e-284 Length: 2040
Score: 2595.00 Matches: 483
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-980-468-2 (1-483) x AAF25729 (1-2040)

QY 1..MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThrTrpSerLysTyrSerVal 20
DB 176 ACGCCCTCGTTACCGACTTCTGAACTTCTGGGCACGACATGAGCAAGTACAGCGTG 235
QY 21 TyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLysValSer 40

DB 236 TACACCCATAGCTATGCTGGAAACTATGGGCCTACTTTGAAGCAGCCAAAAGGTTTCT 295
QY 41 AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSerValGlnAspLysLysPro 60
DB 296 GCTCAAGGTAAACTGCGGGACAGACACTGAGACAGAGATCGGTGCAGGACAAAAGCCA 355
QY 61 GlyThrTyrSerLeuAlaAspValAlaSerHisAspArgProGlyAspCysTrpMetile 80
DB 356 GGCACCTTACTCTCTGGCCGATGTGCTTCTCACGACAGCCCTGGAGACTGCTGGATGATC 415
QY 81 ValLysGluLysValTyrAspIleSerArgPheAlaAspAspHisProGlyGlyThrVal 100
DB 416 GTCAAAGAGAGAGGTGTATGATATTAGCCGTTTTTGGGACGACACCCTGGAGGACGGTA 475
QY 101 IleSerThrTyrPheGlyArgAspGlyThrAspValPheAlaThrPheHisProProAla 120
DB 476 ATTAGCACCTACTTTGGCGGGATGGCACAGACGTTTTTCGCAACATTCCATCCACCTGCC 535
QY 121 AlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAlaArgGluProLeuAsp 140
DB 536 GCATGGAAGCAACTCAATGACTACTACTATTGGAGACTTGCTAGGAGAGCCCTTGAT 595
QY 141 GluLeuLysAspTyrArgAspMetArgAlaGluPheValArgGluGlyLeuPheLys 160
DB 596 GAATTGCTTAAAGACTACAGAGATATGAGAGCCGAGTTTGTAGAGAGGGCTTTTCAAG 655
QY 161 SerSerLysAlaTrpPheLeuGlnThrLeuLeuAsnAlaAlaLeuPheAlaAlaSer 180
DB 656 AGTTCCAAAGGCCCTCGTTCTGCTTACAGACTCTGATTAATGTCAGCTCTCTTTGCTGGAGC 715
QY 181 IleAlaThrIleCysTyrAspLysSerTyrTrpTrpAlaIleValLeuSerAlaSerLeuMet 200
DB 716 ATTGGCACTATCTGTTACGACAAGAGTTACTGGGCTATTGTGTGTAGCCAGTTTGATG 775
QY 201 GlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPheLeuHisGlnValPhe 220
DB 776 GGTCTCTTCGTCCAACAGTGTGGATGGCTTGGCCATGATTCTCTTCATCAACAGGTCTTT 835
QY 221 GluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGlyAsnCysValLeuGlyPhe 240
DB 836 GAGAACCGTACCGGAACTCCTTCTTTGGCTATTGTTGGCAATTGCGTGTCTGGCTTT 895
QY 241 SerValSerTrpTrpArgThrLysHisAsnIleHisHisThrAlaProAsnGluCysAsp 260
DB 896 AGTGTATCAUGGTGGAGGACGAGCAACACATTCATCTGCTCCGAATGAGTGGAC 955
QY 261 GluGlnTyrThrProLeuAspGluAspIleAspThrLeuProIleIleAlaTrpSerLys 280
DB 956 GAACAGTACACACCTCTAGACGAGACATTGATCTCTCCCATCTATGCTCTGGAGCAAG 1015
QY 281 GluIleLeuAlaThrValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyr 300
DB 1016 GAAATTTGGCCACCCTTGAGAGCAAGAGAAATTTGCGAGTGTCTTCAATATCAGCACTAC 1075
QY 301 MetIleLeuProLeuPheMetAlaArgTyrSerTrpThrPheGlySerLeuLeuPhe 320
DB 1076 ATGATTCTGCTCTATTGTTTCATGGCCCGGTACAGTTGGACTTTTGGAAAGTTTGTCTTC 1135
QY 321 ThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGlyThrValAlaPhe 340
DB 1136 ACATTCAATCTCTGATTGAGCAGCAGCAAGGGATTGATAGAGAGGGAACAGTTGCTTTT 1195
QY 341 HisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuProGlyValAlaLysProLeu 360
DB 1196 CACTACGCTGGTTCAAGTTGGGCTGCGTTCCATATTTTGCCGGGTGTCGCTAAGCCTCTT 1255
QY 361 AlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuGlyPheValPheThrLeu 380
DB 1256 GGTGGATGGTAGCAACTGAGCTTGTGGCCGGTTTGTGTGGGATTGCTGTTTACGTTG 1315
QY 381 SerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheValArgAlaGlnValIle 400

Db 1316 AGTCACAAATGGAAGGAGGTTTACAAATGAATCGAAGGACTTCGTGAGAGCCAGGTTATT 1375
Qy 401 ThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThr 420
Db 1376 ACCACCGTAACACCCAGCGAGGCTGTTCAACGATTGGTTCACTGGGGGACTCGACACC 1435
Qy 421 GlnIleGluHisLeuPheProThrMetProArgHisAsnTyrProLysIleAlaPro 440
Db 1436 CAGATTGAGCATCACCTGTTTCCAAATGCCCAGGCACAACTACCCCAAGATCGCACCT 1495
Qy 441 GlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsnValSerValGly 460
Db 1496 CAGGTCGAGGCTCTTTGCAAGAACGACGCGCTCGAGTACGATAATGTCCTCGTGTGGT 1555
Qy 461 AlaSerValAlaValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeu 480
Db 1556 GCCTGTGTCGGGTTGTGAAGCGGCTCAAGGAAATTGCTGATGAGCGTCAATTCCGGCTT 1615
Qy 481 HisAlaHis 483
Db 1616 CACGCTCAC 1624

RESULT 3
AAAF25734
ID AAF25734 standard; DNA; 2160 BP.
XX
AC AAF25734;
XX
DT 06-APR-2001 (first entry)
XX
DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 11.
XX
KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic; ds.
XX
OS Ceratodon purpureus.

XX
EH Location/Qualifiers
FT CDS
FT 159..1721
FT /*tag= a
FT /product= "delta6-acetylenase/delta6-desaturase"

XX
PN WO2000075341-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-EP005274.
XX
PR 07-JUN-1999; 99DE-01025718.
PR 22-DEC-1999; 99DE-01062409.
XX
PA (BADI) BASF AG.
XX
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehring P, Zaehring U;
XX
DR WPI; 2001-112150/12.
DR P-PSDB; AAB46440.
XX
PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
PT producing plant oils with increased content of unsaturated fatty acids.
XX
PS Claim 1a; Page 54-57; 69pp; German.

XX
CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)

CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
CC be used to suppress expression of (II), resulting in oils with increased
CC content of saturated fatty acids

XX
SQ Sequence 2160 BP; 509 A; 481 C; 556 G; 614 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.39e-173 Length: 2160
Score: 1619.00 Matches: 302
Percent Similarity: 76.17% Conservative: 72
Best Local Similarity: 61.51% Mismatches: 101
Query Match: 62.39% Indels: 16
DB: 4 Gaps: 3

US-09-980-468-2 (1-483) x AAF25734 (1-2160)

Qy 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThrTrpSerLysTyrSerVal 20
Db 231 ATGCCCCCTCGTCAGTGACTTCCTAAATGCTCTGGGAACGACTTTGGGCCAGTGGAGTCTT 290
Qy 21 TyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLysLysValSer 40
Db 291 TCCACT---ACATTGCTTTCAAGAGGCTCAGGACTAAGAAACACAGTTCGACATCTCG 347
Qy 41 AlaGln-----GlyLysThrAla 46
Db 348 GTGGAGGCACAAAAGAATCGGTTGCGCGGGGCCAGTTGAGAAATATTCTCAATCGGTT 407
Qy 47 GlyGlnThrLeuArgGlnArgSerValGlnAspLysLysProGlyThrTyrSerLeuAla 66
Db 408 GCGCAGCCCATCAGCGGAGGTGGTGCAGGATAAAAGCCGTTACTTACAGCCTGAAG 467
Qy 67 AspValAlaSerHisAspArgProGlyAspCysTrpMetIleValLysGluLysValTyr 86
Db 468 GATGTAGCTTCGCACGATATGCCCCAGGACTGCTGGATTATAATCAAGAGAGAGTGTAT 527
Qy 87 AspIleSerArgPheAlaAspAspHisProGlyGlyThrValIleSerThrTyrPheGly 106
Db 528 GATGTAGCACCTTCGCTGAGCAGCACCTGGAGGACCGTTATCAACACCTACTTCGGA 587
Qy 107 ArgAspGlyThrAspValPheAlaThrPheHisProProAlaAlaTrpLysGlnLeuAsn 126
Db 588 CGAGACGCCACAGATGTTTCTCTACTTTCCACGCATCCACCTCATGGAAGATTCTTCAG 647
Qy 127 AspTyrTyrIleGlyAspLeuAlaArgGluGluProLeuAspGluLeuLysAspTyr 146
Db 648 AATTTCTACATCGGGAACCTTGTAGGAGGAGCGGACTTTGGAGCTGCTGAAGGAGTAC 707
Qy 147 ArgAspMetArgAlaGluPheValArgGluGlyLeuPheLysSerSerLysAlaTrpPhe 166
Db 708 AGAGAGTTGAGAGCCCTTTTCTTGAGAGAACAGCTTTTCAAGAGATTCCAAATCCTACTAC 767
Qy 167 LeuLeuGlnThrLeuIleAscAlaAlaLeuPheAlaAlaSerIleAlaThrIleCysTyr 186
Db 768 CTTTTCAGAGACTCTCAATAATGTTTCCATTGTTGCCACAAGCATTTGCCGATAATCAGTCTG 827
Qy 187 AspLysSerTyrTrpAlaIleValLeuSerAlaSerLeuMetGlyLeuPheValGlnGln 206
Db 828 TACAAGCTTACCGGGCGGTTCTGTATCAGCCAGTTTGTATGGGCGTTTATTTCACACAG 887
Qy 207 CysGlyTrpLeuAlaHisAspPheLeuHisGlnGlnValPheGluAsnArgThrAlaAsn 226
Db 888 TGCGGATGGTGTCTCAGGATTTTCTACACCATCAGSTATTTTGAGACACGCTGGCTCAAT 947
Qy 227 SerPhePheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTrpArg 246
Db 948 GACGTTGTTGCTATGTGGTCGGAACGTTGTTCTGGGATTTCAGTCTCGTGGTGAAG 1007

Qy 247 ThrLysHisAsnIleHisHisThrAlaProAsnGluCysAspGluGlnTyrThrProLeu 266
Dd 1008 ACCAAGCACAACCTGCATCATGCTGCTCGAATGAATCGACCAAAAGTACACACCGATT 1067
Qy 267 AspGluAspIleAspThrLeuProIleAlaTyrSerLysGluIleLeuAlaThrVal 286
Dd 1068 GATGAGATATTGATCTCTCCCATCATGCTTGGAGTAAAGATCTCTTGGCCACTGTT 1127
Qy 287 GluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeuProLeuLeu 306
Dd 1128 GAGAGCAGACCATGTTGCGAGTCTTCAGTACCAGCACCTATTCTTTTCTTTTCTTTG 1187
Qy 307 PheMetAlaArgTyrSerTyrThrPheGlySerLeuLeuPheThrPheAsnProAspLeu 326
Dd 1188 ACGTTTGGCGGGGAGTATTGGCTATTGAGCGCGGCTTCACCTCAGGCCCGAGTTG 1247
Qy 327 SerThrThrLysGlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTyrPheSer 346
Dd 1248 ACCCTTGGCGAGAGCTTTTGGAGAGGGGAACGATGGCTTTGCACTACATTTGGTTTAAAT 1307
Qy 347 TrpAlaAlaPheHisIleLeuProGlyValAlaLysProLeuAlaTyrMetValAlaThr 366
Dd 1308 AGTGTTCGTTTATCTGCTCCCGGA---TGGAAACCAAGTGTATGATGGATGGTTCAGC 1364
Qy 367 GluLeuValAlaGlyLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGlu 386
Dd 1365 GAGCTCATGCTGCTGCTTCTGCTGGGATCGTATTGTTACTCAGTCACATGGAATGGAG 1424
Qy 387 ValTyrAsnGluSerLysAspPheValArgAlaGlnValIleThrThrArgAsnThrLys 406
Dd 1425 GTGTACAATACGTCAAAGGACTTCGGAAATGCCAGATTGCATCGACTCGGCACATCAA 1484
Qy 407 ArgGlyTrpPheAsnAspTyrPheThrGlyLeuAspThrGlnIleGluHisLeu 426
Dd 1485 GCAGGGGTGTTAATGATTGTTTCCCGGAGGTCTCAACAGACAGATTGAGCATCATCTA 1544
Qy 427 PheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCys 446
Dd 1545 TTTTCCAAACGATGCCAGGCACAACTTATAAAATTTCTCTCAGCTGAGACATTTGTGC 1604
Qy 447 LysLysHisGlyLeuGluTyrAspAsnValSerValGlyAlaSerValAlaValVal 466
Dd 1605 AAGAAGCATGCACTGCTCTACGAAGACGTGAGCATGGCTTCGGGCACTTACCGGGTTTG 1664
Qy 467 LysAlaLeuLysGluIleAlaAspGluAlaSer 477
Dd 1665 AAAACACITTAGGACGTTGCCGATGCTGCTTCA 1697

RESULT 4
ABV74260
ID ABV74260 standard; cDNA; 1578 BP.

AC ABV74260;
XX 28-MAR-2003 (first entry)
DE Physcomitrella patens desaturase encoding cDNA SEQ ID NO 7.
KW Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
KW gene; ss.
OS Physcomitrella patens.
XX Key Location/Qualifiers
FH 1. .1578
FT /tag= a
FT /product= "desaturase"
XX DE10102337-A1.
XX 25-JUL-2002.

XX 19-JAN-2001; 2001DE-01002337.
XX 19-JAN-2001; 2001DE-01002337.
XX (BADI) BASF PLANT SCI GMBH.
PI Lerchl J, Renz A, Heinz E, Domerque F, Zaehring U;
XX WPI; 2002-644810/70.
DR P-PSDB; ABB98277.
XX Preparing ester containing polyunsaturated fatty acids, useful e.g. in
PT animal or human nutrition, by transforming organism with desaturase gene
PT from Phaeodactylum tricornatum.
XX Example 15; Page 60-63; 182pp; German.
XX The invention relates to preparing (M1) fatty acid esters (I) with an
CC increased content of polyunsaturated fatty acids (II) with at least two
CC double bonds by introducing into a (I)-producing organism a specific
CC nucleic acid (A). (M1) is useful for preparing ester containing
CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
CC produced by (M1) are used in animal and human nutrition, cosmetics and
CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
CC the blood and to protect against heart disease. Cells that express (A)
CC are also used to identify (ant)agonists of desaturases, e.g. for
CC modulating the yield and rate of production of particular fine chemicals
CC in microorganisms (claimed). Also (A) and derived proteins can be used as
CC markers of specific genomic regions and in evolutionary/protein
CC structural studies. (M1) is suitable for large scale production (no known
CC bioengineering method can produce (II) on a useful scale). The present
CC sequence is that of a Physcomitrella patens desaturase encoding cDNA used
CC as the (A) component of the invention in producing transgenic (I) -
CC producing organisms
XX Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 3 U; 0 Other;

Alignment Scores:

Pred. No.: 4.9e-157 Length: 1578
Score: 1475.00 Matches: 281
Percent Similarity: 69.88% Conservative: 74
Best Local Similarity: 55.31% Mismatches: 117
Query Match: 56.84% Indels: 36
DB: 6 Gaps: 6

US-09-980-468-2 (1-483) x ABV74260 (1-1578)

Qy 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TrpSerLys 17
Dd 73 ATGTCTCTCTTCAGCGACTTCTTCAGTTATGTGTCTTCAACTGTTGTTGCGTGAGCGTA 132
Qy 18 TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
Dd 133 CACAGTATACAACTTTGAAG-----CGCCTGACGAGTAAGAAG 171
Qy 38 LysValSer----- 40
Dd 172 CGTGTTCGGAAGCGCTGCCGTGCAATGTATATCAGCTGAAGTTCAGAGAAATTCGAGT 231
Qy 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54
Dd 232 ACCCAGGGAACCTCGGAGGCACTCGCAGAAATCAGTCGTGAAGCCCCCAGAGACGAAGTCA 291
Qy 55 ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
Dd 292 TCTCAGTGAAGAGG---TCGACACACCCCTATCAGAAAGTAGCAGTACACACAGGCCA 348
Qy 75 GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94
Dd 349 AGCGATTGCTGGATTGTTGTAACAAACAAAGGTGTATGATGTTTCCCAATTTTGGGACGAG 408
Qy 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114

Db 409 CATCCCGGAGGATCAGTTATTAGTACTATTATTTGGACGACGGCACAGATGTTTCTCT 468
QY 115 ThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla 134
Db 469 AGTTTTCATGCAGCTTCTACATCGGAAATCTTCAAGACTTTTACATTGGTGACGTGGAG 528
QY 135 ArgGluGluProLeuAspGluLeuLeuLysAspTyrArgAspMetArgAlaGluPheVal 154
Db 529 AGGTTGAGSCCGACTCCAGAGCTGCTGAAGATTTCCGAGAATGAGAGCTCTTTCTCTCS 588
QY 155 ArgGluGlyLeuPheLysSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla 174
Db 589 AGGAGCAACTTTTCAAAAGTTGAAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTA 648
QY 175 AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal 194
Db 649 SCTATTTTCTGGAGCATTCGAATATATGTTGGAGCAAGACTATTTCAGCGGTTTTS 708
QY 195 LeuSerAlaSerLeuXetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe 214
Db 709 GCTTCAGCTTGTATGRTGGCTCTGTGTTTCCACAGTGGGATGGCTATCCCATGATTTT 768
QY 215 LeuHisGlnGlnWalPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly 234
Db 769 CTCCACAATCAGGTGCTTGACACACGCTGGCTTAATGAAGTTGTGGGTATGTATCGGC 828
QY 235 AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisHisThr 254
Db 829 AACGCCGTTCTGGGCTTTAGTACAGGGTGGTGAAGAGGAGACATAACCTTCATCATGCT 888
QY 255 AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
Db 889 GCTCCAAATGAATCGATCAGACTTACCAACCAATTTGATGAGATATTTGATCTCTCCC 948
QY 275 IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal 294
Db 949 CTCAATGCTGGAGCAAGGACATACTGGCCACAGTTGAGAAATAAGACATTCTTGGCAATC 1008
QY 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr 314
Db 1009 CTCCAATACCAGCATCTGTTCTTCATGGGTCTGTTATTTTTCGCCCGTGTAGTTGGTCT 1068
QY 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
Db 1069 TTTGGAGCTGGAGATATACCTCTACAGCAGTGTCTCACCTGTCTGACAGGTTGTGGAG 1128
QY 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
Db 1129 AAGGGAACGTTCTGTCTTCACTACTTTTGGTTCGTCGGGACAGCGTGTATCTTCTCCCT 1188
QY 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374
Db 1189 GGT--TGAAGCCATTAGTATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1245
QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
Db 1246 GCCTTTGCTATTGTACTTAGCCACATGGGATGGGATGGGATGGGATGGGATGGGATGGG 1305
QY 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
Db 1306 GTGAGTGCACAGATCGTATCCACGCGGATATCAAGGAAACATATTCAACGACTGGTTC 1365
QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHisAsn 434
Db 1366 ACTGGTGGCCTTAACAGGCAATAGAGCATCTCTTTTCCCAACAATGCCAGGCATATT 1425
QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
Db 1426 TTAAACAAAATAGCACCTAGAGTGGAGGTGTTCTGTGAAGAAACACGGTCTGGTGTACGAA 1485
QY 455 AsnValSerValValGlyAlaSerValAlaValLysAlaLeuLysGluIleAlaAsp 474

Db 1486 GACSTATCTATTGCTACCGGCACCTGCAAGGTTTGAAGCAATTGAAGGAGTCGCG--- 1542
QY 475 GluAlaSerIleArgLeuHisAla 482
Db 1543 GAGGCTCGGCAGAGCAGCATGCT 1566
RESULT 5
ABQ76782
ID ABQ76782 standard; cDNA; 1578 BP.
XX
AC ABQ76782;
XX 25-MAR-2003 (first entry)
DT
DE P. patens D6 desaturase cDNA SEQ ID 7.
XX
KW Promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific; gene; ss.
XX
OS Physcomitrella patens.
XX
FH Key Location/Qualifiers
FT CDS 1..1578
FT /*tag= a
FT /product= "D6 desaturase"
XX
DE10102338-Al.
XX 25-JUL-2002.
XX 19-JAN-2001; 2001DE-01002338.
XX 19-JAN-2001; 2001DE-01002338.
XX (BADI) BASF PLANT SCI GMBH.
PI Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
XX WPI; 2002-675961/73.
DR P-PSDB; ABG73602.
XX
ES New expression cassette for plant genes, useful for preparing transgenic plants that have increased production of polyunsaturated fatty acids.
XX Example 17; Page 64-67; 188pp; German.
XX This invention describes novel expression cassette (EC) containing at least one each of plant promoter (p) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (L1-P-SG-L2)_n where L1 = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a (non-)functional nucleic acid in the vector. Transgenic plants e.g linseed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (PUFA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. PUFA are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression cassettes of the invention provide increased and more efficient production of fine chemicals (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the invention
XX
SQ Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.9e-157 Length: 1578
Score: 1475.90 Matches: 281
Percent Similarity: 69.88% Conservative: 74

Best Local Similarity: 55.31%				Mismatches: 117			
Query Match: 56.84%				Indels: 36			
DB: 6				Gaps: 6			
US-09-980-468-2 (1-483) x ABQ76782 (1-1578)							
QY	1	MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TrpSerLys	17				
Db	73	ATGTCCTCTTCAGCGACTTCTTCAGTTATCTGTCTTCAACTGTTGGTTCGTGGACGTA	132				
QY	18	TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys	37				
Db	133	CACAGTATACAACTTTGAAG-----CGCCTGACGAGTAAGAAG	171				
QY	38	LysValSer-----	40				
Db	172	CGTGTTCGGAAGCGCTGCCGTGCAATGTATATCAGCTGAAGTTCAGAGAAATTCGAGT	231				
QY	41	-----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer	54				
Db	232	ACCCAGGGAACCTCGGAGGCACTCGCAGAAATCAGTCGTGAAGCCCCACGAGACGAAGTCA	291				
QY	55	ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro	74				
Db	292	TCTCAGTGGAGAAG--TCGACACACCCCTATCAGAAGTAGCAGTACACAACAAGCCA	348				
QY	75	GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp	94				
Db	349	AGCGATTGCTGGATGTTGTAAAAACAAGGTGTATGATGTTTCCAAATTTTCGGACGAG	408				
QY	95	HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla	114				
Db	409	CATCCCGGAGGATCAGTTATTAGTACTTATTTGGACGAGACGGCACACATGTTTCTCT	468				
QY	115	ThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla	134				
Db	469	AGTTTTTCAGCTTCTACATGGAAATTTCTTCAAGACTTTTACATTTGGTACGTGGAG	528				
QY	135	ArgGluGlnProLeuAspGluLeuLysAspTyrArgAspMetArgAlaGluPheVal	154				
Db	529	AGGGTGGAGCCGACTCCAGAGCTGCTGAAGAATTTCCGAGAATAGAGCTCTTTTCCTG	588				
QY	155	ArgGluGlyLeuPheLysSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla	174				
Db	589	AGGGAGCAACTTTCAAAGTTCCGAATTTCTACTATGTTATGAAGCTGCTCACGAATGTT	648				
QY	175	AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal	194				
Db	649	GCTATTTTGTCTCGAGCATTGCAATAATATGTTGGACGAAGACTATTTCAGCGGTTTG	708				
QY	195	LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe	214				
Db	709	GCTTCAGCTTGATGGCTCTGTGTTTCCACAGTCGGATGGGTATCCCATGATTTT	768				
QY	215	LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly	234				
Db	769	CTCCACAAATCAGGTGTTTGAGACACCGCTGGCTTAATGAAGTTGTTCGGGTATGTGATCGGC	828				
QY	235	AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisHisThr	254				
Db	829	AACGCCGTCTCGGGTTTAGTACAGGGTGGTGAAGGAGAGCAATAACCTTCATCATGCT	888				
QY	255	AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro	274				
Db	889	GCTCCAAATGAATCGATCAGACTTACCAACCAATTTGATGAAGATATTGATCTCTCCC	948				
QY	275	IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal	294				
Db	949	CTCATTTGCTGGAGCAAGGACATCTGCCCCACAGTTGAGAATAAGACATTTCTTGGCAATC	1008				
QY	295	LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr	314				
Db	1009	CTCCAAATCCAGCATCTGTTCTTCATGGGTCTGTTATTTTTCGCCCGGTAGTTGGCTC	1068				

QY	315	PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu	334
Db	1069	TTTTGGAGCTGGAGATATACCTCTACAGCAGTGTCTCACCTGTGACAGGTTGTTGGAG	1128
QY	335	LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro	354
Db	1129	AAGGGAACCTGTTCTGTTCACACTTTTGGTTCGTGGGACAGCGTCTATCTTCCTC	1188
QY	355	GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeu	374
Db	1189	GGT---TGGAAAGCCATTAGTATGGATGGGCGGTGACTGAGCTCATGTCCGGCATGTGCTG	1245
QY	375	GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe	394
Db	1246	GGCTTTGTATTGTACTTAGCCACAATGGGATGGAGGTTTATAATTCTCTAAAGAATTC	1305
QY	395	ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe	414
Db	1306	GTGAGTGCACAGATCGTATCCACACGGGATATCAAAGGAAACATATTCAACGACTGTT	1365
QY	415	ThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHisAsn	434
Db	1366	ACTGGTGGCCTTAACAGGCAATAGAGCATCATCTTTCCCAACAATGCCAGGCAAT	1425
QY	435	TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp	454
Db	1426	TTAAACAAATAGCACCTAGAGTGGAGTGTCTCTGAAGAAACACCGTCTGGTGTACGAA	1485
QY	455	AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp	474
Db	1486	GACGTATCTATTGTACCGGCACCTTGCAGGTTTTTGAAGCATTTGAAGGAAGTCGG---	1542
QY	475	GluAlaSerIleArgLeuHisAla	482
Db	1543	GAGGCTGGCGCAGACGACGATGCT	1566

RESULT 6
AAF26040
ID AAF26040 standard; cDNA; 2012 BP.
XX
AC AAF26040;
DT 23-APR-2001 (first entry)
XX
DE P. patens delta6-desaturase cDNA.
XX
KW Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;
KW fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;
KW agricultural chemical; ds.
OS Physcomitrella patens.
XX
FH Key Location/Qualifiers
FT CDS 319..1896
FT /*tag= a
FT /product= "delta6-desaturase"
XX
PN WC200102591-A1.
PD 11-JAN-2001.
XX
PF 04-JUL-2000; 2000WO-EP006223.
XX
PR 06-JUL-1999; 99US-00347531.
PR 30-JUN-2000; 2000DE-01030976.
XX
PA (BADI } BASF AG.
PI Heinz E. Girke T. Scheffler J. Da Costa E SilvaO;
XX
DR WPI; 2001-123117/13.
DR P-PSDB; AAB46810.

Production of unsaturated fatty acids, useful e.g. in nutrition, cosmetics or pharmaceuticals, in organisms transformed with *Physcomitrella patens* δ - α -6-desaturase nucleic acid.

This invention describes a novel preparation of unsaturated fatty acids (I) by introducing into an organism at least one isolated nucleic acid (II) that encodes a polypeptide (III) with Delta6-desaturase activity. Organisms that contain at least 1 wt. % (I), on total fatty acid content, are then selected. (II) is selected from: (a) a 20-2 bp sequence (S1), defined in the specification, or its equivalents within the degeneracy of the genetic code; or (b) derivatives of the sequence of (a) that encode a 525 amino acid polypeptide (S2), defined in the specification, or a polypeptide with at least 50% homology with (S2) and practically the same enzymatic activity. The invention also describes (1) transgenic organisms that contain (II); and (2) oils, lipids and fatty acids produced by the new method. The oils, lipids and fatty acids produced by the transformed organisms are used in human or animal nutrition, cosmetics, pharmaceuticals and agricultural chemicals. (III) can also be used, *in vitro*, for increasing the (I) content of triglycerides. The transgenic organisms have increased contents of (I), or of (I)-containing triglycerides, particularly of gamma-linolenic acid

Sequence 2012 BP; 482 A; 427 C; 553 G; 550 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.08e-157	Length:	2012
Score:	1495.00	Matches:	281
Percent Similarity:	69.88%	Conservative:	74
Best Local Similarity:	55.31%	Mismatches:	117
Query Match:	56.84%	Indels:	36
DB:	4	Gaps:	6

JS-09-980-468-2 (1-483) x AAF26040 (1-2012)

QY	1	MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TrpSerLys	17
DB	391	ATGTCCTCTTCAGCGACTTCCTCAGTATGTTCTTCAACTGTTGGTTCGTGGACGTA	450
QY	18	TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys	37
DB	451	CACAGTATACAACTTTGAAG-----CGCCTGACGAGTAAGAAG	489
QY	38	LysValSer-----	40
DB	490	CGTGTTCGGAAAGCGCTGCCGTGCAATGTATATCAGCTGAAGTTCAGAGAAATTCGAGT	549
QY	41	-----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer	54
DB	550	ACCCAGGGAACCTGGGAGGCACTCCGAGAATCAGTCCTGTAAGCCCAAGACGACGAAGGTCA	609
QY	55	ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro	74
DB	610	TCTCAGTGGAGAAG--TCGACACACCCCTATCAGAAGTAGCAGTACACAACAAGCCA	666
QY	75	GlyAspCysTipMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp	94
DB	667	AGCGATTGCTGGATTGTTGTAATAAACAAAGGTGTATGATGTTTCCAAATTTGCGGACGAG	726
QY	95	HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla	114
DB	727	CATCCCGGAGGATCAGTTATTAGTACTTATTTTGGACGAGACGGCACAGATGTTTCTCT	786
QY	115	ThrPheHisProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla	134
DB	787	AGTTTTTCATGCAGCTTCTACATGGAAAATTTCTTCAAGACTTTTACATTGGTGCAGTGGAG	846
QY	135	ArgGluGluProLeuAspGluLeuLeuLysAspTyrArgAspMetArgAlaGluPheVal	154
DB	847	AGGGTGGAGCCGACTCCAGAGCTGCTGAAGATTTCCGAGAAATGAGAGTCTTTTCTCTG	906

QY	155	ArgGluGlyLeuPheLysSerSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla	174
DB	907	AGGGAGCACTTTTCAAAAGTTCGAAATTGTACTATGTTATGAAGCTGCTCAGCAATGTT	966
QY	175	AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal	194
DB	967	GCTATTTTGTGCGAGCAATTGCATATATATGTTGGAGCAAGACTATTTTTCAGCGGTTTGTG	1026
QY	195	LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe	214
DB	1027	GCTTCAGCTCTGTATGATGGCTCTGTGTTTCCAAACAGTGGGATGGCTATCCCATGATTTT	1086
QY	215	LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly	234
DB	1087	CTCCACAATCAGGTGTTTGAGACACGCTGGCTTAATGAAGTTGTCGGGTATGTGATCGGC	1146
QY	235	AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisHisThr	254
DB	1147	AACGCCGTTCTGGGGTTTAGTACAGGTGGTGGAGAGAGCAATACCTTCATCATGCT	1206
QY	255	AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspLeuAspThrLeuPro	274
DB	1207	GCTCCAAATGAATGCGATCGACTTACCAACCAATTGATGAAGATATTGATACTCTCCCC	1266
QY	275	IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal	294
DB	1267	CTCATTTGCCTGGAGCAAGGACATACCTGCGCACAGTTGAGAAATAGACATTTCTTGGCAATC	1326
QY	295	LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr	314
DB	1327	CTCCAATACCAGCATCTGTTCTTCTCATGGGTCTGTATTATTTTCGCCCCGTGGTAGTTGGCTC	1386
QY	315	PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu	334
DB	1387	TTTTGGAGCTGGAGATATACCTCTACAGCAGTGCTCTCACCTGTGACAGGTTGTTGGAG	1446
QY	335	LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro	354
DB	1447	AAGGGAACCTGTTCTGTTTCACTACTTTTGGTTCTGTCGGGACAGCGTGCTATCTTCTCCCT	1506
QY	355	GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu	374
DB	1507	GGT--TGGAAGCCATTAGTATGGATGCGCGGTGACTGAGCTCATGTCGGGCATGCTGCTG	1563
QY	375	GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe	394
DB	1564	GGCTTTGTATTGTTACTTAGCCACATGGGATGGAGGTTTATATTCGTTCTAAAGAATTC	1623
QY	395	ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe	414
DB	1624	GTGAGTGACAGATCGTATCCACACGGGATATCAAAGGAACAATATTCACAGCTGGTTC	1683
QY	415	ThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHisAsn	434
DB	1684	ACTGGTGGCTTAACAGGCAATAGACATCATCTTTTCCCAACAATGCCAGGCATAAT	1743
QY	435	TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp	454
DB	1744	TTAAACAAAATAGCACCTAGAGTGGAGGTGTTCTGTGAAGAAACACGGTCTGGTGTACGAA	1803
QY	455	AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp	474
DB	1804	GACGTATCTATTGCTACCGGCACCTTGCAAGGTTTGTGAAGCATTTGAAGGAAGTCGCG---	1860
QY	475	GluAlaSerIleArgLeuHisAla	482
DB	1861	GAGGCTGGCGAGCAGCATGCT	1884

RESULT 7
 ABX13450
 ID ABX13450 standard; DNA; 2012 BP.
 XX
 AC ABX13450;

QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
DB 1564 GGCTTGTGATTGTACTTAGCCACAATGGGATGGAGGTTTATATAATCGTCTAAAGAATTC 1623
QY 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
DB 1624 GTGAGTGCACAGATCGTATCCACACGGGATATCAAAAGGAACATATCTCAACGACTGGTTC 1683
QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsn 434
DB 1684 ACTGGTGGCTTACAGGCAAAATAGAGCATCTCTTCCCAACATATGCCAGGCATAAT 1743
QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
DB 1744 TTAACAAATAAGCACCTAGAGTGGAGGTCTCTGTAAAGAACACGGTCTGGTGTACGAA 1803
QY 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
DB 1804 GACGTATCTATTGCTACCGCACTTGCAAGGTTTGAAGCATTGAAGGAAGTCGCG--- 1860
QY 475 GluAlaSerIleArgLeuHisAla 482
DB 1861 GAGGCTGCGGAGAGCAGCATGCT 1884

RESULT 8
ABV74274
ID ABV74274 standard; DNA; 15430 BP.
XX
AC ABV74274;
XX
DT 07-AUG-2003 (revised)
DT 28-MAR-2003 (first entry)
XX
DE Plant specific expression vector expressing desaturase SEQ ID NO 25.
XX
KW Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
KW plant; elongase; gene; ds.
XX
OS Phaeodactylum tricornutum.
OS Physcomitrella patens.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 11543..12415
FT /*tag= a
FT /product= "elongase"
FT /note= "ABB98278"
FT CDS 13313..14890
FT /*tag= b
FT /product= "desaturase"
FT /note= "ABB98277"
XX
DE10102337-A1.
XX
PD 25-JUL-2002.
XX
PF 19-JAN-2001; 2001DE-0102337.
XX
PR 19-JAN-2001; 2001DE-0102337.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Lerchl J, Renz A, Heinz E, Domerque F, Zaehringer U;
XX
DR WPI; 2002-64481C/70.
DR P-PSDB; ABB98278, ABB98277.
XX
PT Preparing ester containing polyunsaturated fatty acids, useful e.g. in
PT animal or human nutrition, by transforming organism with desaturase gene
PT from Phaeodactylum tricornutum.

XX
PS
XX
CC The invention relates to preparing (M1) fatty acid esters (I) with an
CC increased content of polyunsaturated fatty acids (II) with at least two
CC double bonds by introducing into a (i)-producing organism a specific
CC nucleic acid (A). (M1) is useful for preparing ester containing
CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
CC produced by (M1) are used in animal and human nutrition, cosmetics and
CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
CC the blood and to protect against heart disease. Cells that express (A)
CC are also used to identify (ant)agonists of desaturases, e.g. for
CC modulating the yield and rate of production of particular fine chemicals
CC in microorganisms (claimed). Also (A) and derived proteins can be used as
CC markers of specific genomic regions and in evolutionary/protein
CC structural studies. (M1) is suitable for large scale production (no known
CC bioengineering method can produce (II) on a useful scale). The present
CC sequence is that of the pUC19 based plant specific expression vector
CC (ABV74272) expressing the Physcomitrella patens elongase (ABB98278) and
CC the Phaeodactylum tricornutum desaturase (ABB98277) of the invention.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 15430 BP; 3733 A; 3826 C; 4153 G; 3718 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.55e-155 Length: 15430
Score: 1475.00 Matches: 281
Percent Similarity: 69.88% Conservative: 74
Best Local Similarity: 55.31% Mismatches: 117
Query Match: 56.84% Indels: 36
DB: 6 Gaps: 6

US-09-980-468-2 (1-483) x ABV74274 (1-15430)

QY 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TrpSerLys 17
DB 13385 ATGTCTCTCTTCAGCGACTTCTTCAGTTATGTGTCTTCAACTGTGGTTCGTGAGCGTA 13444
QY 18 TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
DB 13445 CACAGTATACAACTTTGAAG-----CGCCTGACGAGTANGAAG 13483
QY 38 LysValSer----- 40
DB 13484 CGTGTTCGGAAAGCGCTGCCGTGCAATGATATATCAGTGAAGTTCAGAGAAATTCGAGT 13543
QY 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54
DB 13544 ACCCAGGGAAGTCCGAGGCACTCGCAGATCAGTCTGTGAAGCCCGAGACGAGGATCA 13603
QY 55 ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
DB 13604 TCTCAGTGGAGAAG--TCGACACACCCCTATCAGAGTAGCAGTACACAAAGCCA 13660
QY 75 GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94
DB 13661 AGCGATTGCTGGATTGTTGTAATAAACAAAGGTGTATGATGTTTCCAAATTTGCGGACGAG 13720
QY 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114
DB 13721 CATCCCGGAGGATCAGTTATTAGTACTATTATTGGACGAGACGGCACAGATGTTTCTCT 13780
QY 115 ThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrTrpIleGlyAspLeuAla 134
DB 13781 AGTTTTCATGAGCTTCTACATGGAAAATTTCTCAAGACTTTTACATTGGTGACGTGGAG 13840
QY 135 ArgGluGluProLeuAspGluLeuLysAspTyrArgAspTyrArgAlaGluPheVal 154
DB 13841 AGGGTGGAGCCGACTCCAGAGCTGCTGAAGATTTCCGAGAAATGAGAGCTCTTTTCTCTG 13900
QY 155 ArgGluGlyLeuPheLysSerSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla 174
DB 13901 AGGGAGCAACTTTTCAAAAGTTTCGAAATTTGCTACTATGTTATGAAGCTGCTCAGCAATGTT 13960

[illegible]

DE	pb-DHGLA encoding P. patens delta6 elongase and delta6 desaturase.
XX	
KW	Promoter; expression cassette; structural gene; plant; transgenic;
KW	linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW	animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW	heart disease; seed-specific; gene; ds.
XX	
OS	Physcomitrella patens.
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	11543. .12415
FT	/*tag= a
FT	/product= "delta6 elongase"
FT	13313. .14890
FT	/*tag= b
FT	/product= "delta6 desaturase"
FT	

DE1010233B-A1.

25-JUL-2002.

19-JAN-2001; 2001DE-01002338.

19-JAN-2001; 2001DE-01002338.

(EADI) BASF PLANT SCI GMBH.

Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J, J

WPI; 2002-675961/73.

P-PSDB; ABG73606, ABG73607.

New expression cassette for plant genes, useful for preparing transgenic plants that have increased production of polyunsaturated fatty acids.

Example 13; Page 140-154; 188pp; German.

This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (L1-P-SG-L2)_n where L1 = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a (non-)functional nucleic acid in the vector. Transgenic plants e.g linseed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (PUFA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. PUFA are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression cassettes of the invention provide increased and more efficient production of fine chemicals (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the invention

Sequence 15430 BP; 3733 A; 3826 C; 4153 G; 3718 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.55e-155	Length:	15430
Score:	1475.00	Matches:	281
Percent Similarity:	69.88%	Conservative:	74
Best Local Similarity:	55.31%	Mismatches:	117
Query Match:	56.84%	Indels:	36
DB:	6	Gaps:	6

US-09-980-468-2 (1-483) x ABQ76796 (1-15433)

1 MetAlaLeuValThrAspPheLeuAsnPteLeuGlyThr-----TrpSerLys 17

Db 13385 ATGTCCTCTTCAGCGACTCTTCAGTTATGTGTCCTCAACTGTTGGTTCGGAGCGTA 13444

RESULT 9
ABQ76796

ID ABQ76796 standard; DNA; 15430 BP.

AC ABQ76796;

DT 25-MAR-2003 (first entry)

XX

QY 18 TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
:::|||||
Db 13445 CACAGTATACAAACCTTTGAAG-----CGCCTGACGAGTAAGAAG 13483

QY 38 LysValSer-----40
Db 13484 CGTGTTTCGGAAAGCGCTGCCGTGCAATGTATATCAGCTGAAGTTTCAGAGAAATTCGAGT 13543

QY 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54
Db 13544 ACCCAGGAACTGCGGAGGCACCTCGCAGAATCAGTCGTGAAGCCCCACGAGACGAAGGTCA 13603

QY 55 ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
Db 13604 TCTCAGTGGAGAAG--TCGACACACCCCTATCAGAAGTAGCAGTACACACAAGCCA 13660

QY 75 GlyAspCysTrpXetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94
Db 13661 AGCGATTGCTGGATTGTTGTAAAAACAAGGTGTATGATGTTTCCAAATTTTCGGGACGAG 13720

QY 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114
Db 13721 CATCCCGGAGGATCAGTTATTAGTACTTATTTTGGACGAGACGGCACAGATGTTTCTCT 13780

QY 115 ThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla 134
Db 13781 AGTTTTCATGCAGCTTCTACATGGAAATCTTCAAGACTTTTTACATTGGTGACGTGGAG 13840

QY 135 ArgGluGluProLeuAspGluLeuLysAspTyrArgAspMetArgAlaGluPheVal 154
Db 13841 AGGGTGGAGCCGACTCCAGAGCTGCTGAAGAATTCGAGAAATCCGAGAAATGAGAGCTCTTTTCCTG 13900

QY 155 ArgGluGlyLeuPheLysSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla 174
Db 13901 AGGGAGCAACTTTTCAAAAGTTCGAAATGTACTATGTTATGAAGCTGCTCAGCAATGTT 13960

QY 175 AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal 194
Db 13961 GCTATTTTGTCTCGAGCATTTGCAATAATATGTGGACGACGACTATTTTTCAGCGGTTTG 14020

QY 195 LeuSerAlaSerLeuMetGlyLeuPheValGlnCysGlyTrpLeuAlaHisAspPhe 214
Db 14021 GCTTCAGCTTGATGATGGCTCTGTGTTTCCACAGCTGCGGATGGCTATCCCATGATTTT 14080

QY 215 LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly 234
Db 14081 CTCACAAATCAGGTGTTTGAGACACGCTGGCTTAAATCAAGTTGTCCGGTATGTGATCGGC 14140

QY 235 AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisThr 254
Db 14141 AACGCCGTTCTGGGTTTAGTACAGGGTGGTGGAGAGAGAGACATAACCTTCATCATGCT 14200

QY 255 AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
Db 14201 GCTCCAAATGAATGGATCAGACTTACCACCAATGATGAAGATATTGATCTCTCCCC 14260

QY 275 IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal 294
Db 14261 CTCATTGCCTGGAGCAAGGACATACCTGCGCCACAGTTGAGAATAAGACATTCTTCGAATC 14320

QY 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuPhePheMetAlaArgTyrSerTrpThr 314
Db 14321 CTCCAATACCAGCATCTGTTCTTTCATGGGTCTGTATTTTTCGCCCGTGGTAGTTGGCTC 14380

QY 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
Db 14381 TTTTGGAGCTGGAGATATACCTCTACAGCAGTGTCTCACCTGTGACAGGTTGTTGGAG 14440

QY 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
Db 14441 AAGGGAACTGTTCTGTTTCACTACTTTTGGTTCGTGGGACAGCGTGTCTCTCTCCCT 14500

QY 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374

Db 14501 GGT---TCGAAGCCATTAGTATGGATGGGGTGACTGAGCTCATGTCCGGCATGCTGCTG 14557

QY 375 GlyPheValPheThrLeuSerHisAspGlyLysGluValTyrAsnGluSerLysAspPhe 394
Db 14558 GGCTTTGTATTGTACTTAGCCACAATGGGATGGAGGTTTATAATTGCTCTAAAGAATTC 14617

QY 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
Db 14618 GTGAGTGCACAGATCGTATCCACACGGGATATCAAGGAAACATATTCAACGACTGGTTC 14677

QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHisAsn 434
Db 14678 ACTGGTGGCCTTAACAGGCAATAGAGCATCATCTTTCCCAACAATGCCAGGCATAT 14737

QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
Db 14738 TTAACAAATAGCACCTAGAGTGGAGGTCTCTGTAAAGAAACCGGTCTGGTGTACGAA 14797

QY 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
Db 14798 GACGTATCTATTGCTACCGGCACCTTGCAAGGTTTGAAGCATTTGAAGGAAAGTCGCG--- 14854

QY 475 GluAlaSerIleArgLeuHisAla 482
Db 14855 GAGGCTGGGCAGACGACGATGCT 14878

RESULT 10
ABV74275
ID ABV74275 standard; DNA; 17752 BP.
XX
AC ABV74275;
XX
DT 07-AUG-2003 (revised)
DT 28-MAR-2003 (first entry)
XX
Plant specific expression vector expressing desaturase SEQ ID NO 28.
DE Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
XX animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
KW plant; elongase; gene; ds.
XX
OS Phaeodactylum tricornutum.
OS Physcomitrella patens.
OS Synthetic.
XX Chimeric.
FH Key Location/Qualifiers
CDS 11543..12415
FT /*tag= a
FT /product= "elongase"
FT /note= "ABB98278"
CDS 13313..14890
FT /*tag= b
FT /product= "desaturase"
FT /note= "ABB98277"
CDS 15791..17200
FT /*tag= c
FT /product= "desaturase"
FT /note= "ABB98274"
XX DE10102337-A1.
PN
XX 25-JUL-2002.
XX
XX 19-JAN-2001; 2001DE-01002337.
PF
XX 19-JAN-2001; 2001DE-01002337.
PR
XX (BADI) BASF PLANT SCI GMBH.
PA
XX Lerchl J, Renz A, Heinz E, Domerque F, Zaehringer U;
PI
XX

DR WPI: 2002-644810/73.
DR P-ESDB; ABB98276, ABB98277, ABB98274.
XX
PT Preparing ester containing polyunsaturated fatty acids, useful e.g. in
PT animal or human nutrition, by transforming organism with desaturase gene
PT from Phaeodactylum tricornutum.
XX
PS Example 11; Page 154-170; 182pp; German.
XX
CC The invention relates to preparing (M1) fatty acid esters (I) with an
CC increased content of polyunsaturated fatty acids (II) with at least two
CC double bonds by introducing into a (I)-producing organism a specific
CC nucleic acid (A). (M1) is useful for preparing ester containing
CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
CC produced by (M1) are used in animal and human nutrition, cosmetics and
CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
CC the blood and to protect against heart disease. Cells that express (A)
CC are also used to identify (ant)agonists of desaturases, e.g. for
CC modulating the yield and rate of production of particular fine chemicals
CC in microorganisms (claimed). Also (A) and derived proteins can be used as
CC markers of specific genomic regions and in evolutionary/protein
CC structural studies. (M1) is suitable for large scale production (no known
CC bioengineering method can produce (II) on a useful scale). The present
CC sequence is that of the pUC19 based plant specific expression vector
CC (ABV74273) expressing the Physcomitrella patens elongase (ABB98278; and
CC the Phaeodactylum tricornutum desaturase (ABB98277 and ABB98274) of the
CC invention. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 17752 BP; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.92e-155 Length: 17752
Score: 1475.00 Matches: 281
Percent Similarity: 69.88% Conservative: 74
Best Local Similarity: 55.31% Mismatches: 117
Query Match: 56.84% Indels: 36
DB: 6 Gaps: 6

US-09-980-468-2 (1-483) x ABV74275 (1-17752)

QY 1 MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----TrpSerLys 17
DB 13385 ATGCTCTCTTCAGCGACTTCTTCAGTATGTGTCTTCAACTGTGTTCTGCGAGCGTA 13444
QY 18 TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
DB 13445 CACAGTATACAACTTTGAAG-----CGCTGACGAGTAAGAAG 13483
QY 38 LysValSer----- 40
DB 13484 CGTGTTCGGAAGCGCTGCGTGCATATATATCATCAGCTGAAGTTTCAGAGAAATTCGAGT 13543
QY 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54
DB 13544 ACCCAGGAACCTCGGAGGCACTCGCAGAAATCAGTCTGTGAAGCCCGCAGACGAGGTCA 13603
QY 55 ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
DB 13604 TCTCAGTGAAGAAG---TCGACACACACCCCTATCAGAAGTAGCAGTACACAAACAGCCA 13660
QY 75 GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94
DB 13661 AGCGATTGCTGGATTGTTGTAATAAACAGAGGTGTATGATGTTTCCAAATTTGCGACGAG 13720
QY 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114
DB 13721 CATCCCGGAGGATCAGTTATTAGTACTATTATTGGACGAGACGCGCAGATGTTTCTCT 13780
QY 115 ThrPheHisProProAlaAlaTyrLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla 134
DB 13781 AGTTTTTCATGACGCTCTACATGGAAAATCTTCAAGACTTTTACATGGTGGTGGAG 13840
QY 135 ArgGluGlnProLeuAspGluLeuLysAspTyrArgAspMetArgAlaGluPheVal 154

DB 13841 AGGGTGGAGCGGACTCCAGAGCTGCTGAAAGATTTCGAGAAATGAGAGCTCTTTCTCTG 13900
QY 155 ArgGluGlyLeuPheLysSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla 174
DB 13901 AGGGAGCAACTTTTCAAAAGTTTCGAAATTGCTACTATGTTATGAGCTGCTCAGGAATGT 13960
QY 175 AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal 194
DB 13961 GCTATTTTGTCTGGAGCATTGCAATAATAATATGTTGGAGCAAGACTATTTTCAGCGTTTG 14020
QY 195 LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe 214
DB 14021 GCTTCAGCTTGATGATGGCTCTGTGTTTCCAAACAGTGGGATGGCTATCCCATGATTTT 14080
QY 215 LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPheGlyTyrLeuPheGly 234
DB 14081 CTCCACAATCAGGTGTTTGAGACACGCTGGCTTAATGAAGTTGTCCGGTATGTCGATCGGC 14140
QY 235 AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisThr 254
DB 14141 AACGCCGTTCTGGGTTTAGTACAGGTGTGTGAAGGAGAGACATAACCTTCATCATGCT 14200
QY 255 AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
DB 14201 GCTCCAAATGAATCGATCAGACTTACCAACCAATTGATGAAGATATTGATACTCTCCC 14260
QY 275 IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal 294
DB 14261 CTCATTGCCCTGGAGCAAGGACATACACTGCGCCACAGTTGAGATAAGACATTCTTGGCAATC 14320
QY 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr 314
DB 14321 CTCCAATACAGCATCTGTTCTTCATGGGTCGTGTTATTTTCGCCCGGTGGTAGTTGGCTC 14380
QY 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
DB 14381 TTTTGGAGCTGGAGATATACCTCTACAGCAGTGTCTCACCTGTGACAGGTTGTTGGAG 14440
QY 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
DB 14441 AAGGGAACCTGTTCTGTTTCACTACTTTTGGTTCGTGCGGACAGCGTGTATCTTCTCCCT 14500
QY 355 GlyValAlaLysProLeuAlaTyrMetValAlaThrGluLeuValAlaGlyLeuLeu 374
DB 14501 GGT---TCGAAGCCATTAGTATGGATGGCGGTGACTGAGCTCATGTCCGGCATGCTGCTG 14557
QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
DB 14558 GGCTTTGTATTGTACTTAGCCACAATGGGATGGAGGTTTATAATTCTCTAAAGAATTTC 14617
QY 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
DB 14618 GTGAGTGACAGATCGTATCCACCGGGATATCAAGGAAACATATTCAACGACTGGTTC 14677
QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsn 434
DB 14678 ACTGGTGGCCTTAACAGGCAARTAGAGCATCATCTTTTCCCAACAATGCCAGGCATATT 14737
QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
DB 14738 TTAACAAAATAGCACCTAGAGTGGAGGTCTCTGTGAAGAACACGGTCTGTGTACGAA 14797
QY 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
DB 14798 GACGTATCTATTGCTACCGGCACTTGCAGGTTTGAAGCATTTGAAGGAAGTCGCG--- 14854
QY 475 GluAlaSerIleArgLeuHisAla 482
DB 14855 GAGGCTGCGGACAGACGATGCT 14878
RESULT 11
ABQ76797

ID ABQ76797 standard; DNA; 17752 BP.
XX
AC ABQ76797;
XX
XX
DT 25-MAR-2003 (first entry)
XX
DE pBAR1 encoding delta6 elongase, delta6 and delta5 desaturase.
XX
KW Promoter; expression cassette; structural gene; plant; transgenic;
KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
KW heart disease; seed-specific; ds.
XX
OS Physcomitrella patens.
OS Phaeodactylum tricornutum.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 11543. 12415
FT CDS
FT /*tag= a
FT /product= "delta6 elongase"
FT /note= "from Physcomitrella patens"
FT CDS 13313. 14890
FT /*tag= b
FT /product= "delta6 desaturase"
FT /note= "from Physcomitrella patens"
FT CDS 15791. 17200
FT /*tag= c
FT /product= "delta2 desaturase"
FT /note= "from Phaeodactylum tricornutum"
XX
DE10102338-A1.
XX
XX
PD 25-JUL-2002.
XX
XX
PF 19-JAN-2001; 2001DE-01002338.
XX
PR 19-JAN-2001; 2001DE-01002338.
XX
XX (BADI) BASF PLANT SCI GMBH.
XX
XX Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
XX WPI; 2002-675961/73.
DR P-PSDB; ABG73608, ABG73609, ABG73610.
XX
PT New expression cassette for plant genes, useful for preparing transgenic
PT plants that have increased production of polyunsaturated fatty acids.
XX
PS Example 13; Page 158-174; 188pp; German.
XX
CC This invention describes novel expression cassette (EC) containing at
CC least one each of plant promoter (P) and structural gene (SG) expressed
CC in plants, flanked by specific restriction enzyme (RE) recognition sites.
CC The EC has the structure (L1-P-SG-L2) n where L1 = is a polylinker
CC (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
CC sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
CC sequences and n = 1-3. The invention discloses a vector containing this
CC EC, an organism containing the EC or the vector and a transgenic plant
CC containing a (non-)functional nucleic acid in the vector. Transgenic
CC plants e.g linseed can be prepared with improved production of fatty acid
CC esters with an increased content of polyunsaturated fatty acids (PUFA),
CC useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
CC PUFA are known to reduce levels of cholesterol in the blood and to
CC protect against heart disease. The expression cassettes of the invention
CC provide increased and more efficient production of fine chemicals
CC (especially PUFA), including seed-specific production. This sequence
CC represents a nucleic acid sequence used to illustrate the method of the
CC invention
XX
SQ Sequence 17752 BP; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;
Alignment Scores:

Pred. No.:	1.92e-155	Length:	17752
Score:	1475.00	Matches:	281
Percent Similarity:	69.88%	Conservative:	74
Best Local Similarity:	55.31%	Mismatches:	117
Query Match:	56.84%	Indels:	36
DB:	6	Gaps:	6
US-09-980-468-2 (1-483) x ABQ76797 (1-17752)			
QY	1	MetAlaLeuValThrAspPheLeuAsnPheLeuGlyThrThr-----	TrpSerLys 17
Db	13385	ATGTCTCTCTTCAGCGACTTCTTCAGTTATGTCTTCACTGTTGGTTCGTGGAGCGTA	13444
QY	18	TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37	
Db	13445	CACAGTATACAACTTTTGAAG-----CGCCTGACGAGTAAGAAG	13483
QY	38	LysValSer-----	40
Db	13484	CGTGTTCGGAAGCGCTGCCGTGCAATGATATATCAGCTGAAGTTCAGAGAAATTCGAGT	13543
QY	41	-----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54	
Db	13544	ACCCAGGGAACTGCGGAGGCACTCGCAGAAATCAGTCTGTGAAGCCACGAGACGAAGTCA	13603
QY	55	ValGlnAspLysLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74	
Db	13604	TCTCAGTGGAGAAG--TCGACACACCCCTATCAGAAGTAGCAGTACACAACAAGCCA	13660
QY	75	GlyAspCysTyrMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94	
Db	13661	AGCGATTGCTGGATTGTTGTAATAAACAAGGTATGATGTTTCCAAATTTTCGGGACGAG	13720
QY	95	HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114	
Db	13721	CATCCCGGAGGATCAGTTATTAGTACTTATTTTGGACGAGACGGCACAGTGTTCCTCT	13780
QY	115	ThrPheHisProProAlaAlaTyrLysGlnLeuAsnAspTyrTyrIleGlyAspLeuAla 134	
Db	13781	AGTTTTTCATGCAGCTTCTACATGGAAAATTCCTCAAGACTTTTACATTGGTGACGTGGAG	13840
QY	135	ArgGluGluProLeuAspGluLeuLysAspTyrArgAspMetArgAlaGluPheVal 154	
Db	13841	AGGGTGGAGCCGACTCCAGAGCTGCTGAAAGATTTCCGAGAATGAGAGCTCTTTTCCTG	13900
QY	155	ArgGluGlyLeuPheLysSerSerLysAlaTyrPheLeuGlnThrLeuIleAsnAla 174	
Db	13901	AGGGAGCAACTTTTCAAAAGTTCGAAATTTGTAATGTTATGTAAGCTGCTCAGCAATGTT	13960
QY	175	AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal 194	
Db	13961	GCTATTTTGTGCGGAGCATTCGCAATAATATGTTGGAGCAGACTATTTTCAGCGGTTTG	14020
QY	195	LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTyrLeuAlaHisAspPhe 214	
Db	14021	GCTTCAGCTGTATGATGGCTCTGTGTTTCCACAGTCGGATGGCTATCCCATGATTTT	14080
QY	215	LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly 234	
Db	14081	CTCCACAATCAGGTGTTTGAGACACGCTGGCTTAATGAAGTTGTCGGGTATGTGATCGGC	14140
QY	235	AsnCysValLeuGlyPheSerValSerTyrTrpArgThrLysHisAsnIleHisHisThr 254	
Db	14141	AACGCCGTTCTGGGGTTTAGTACAGGGTGGTGAAGGAGAAGCATACCTTCATCATGCT	14200
QY	255	AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274	
Db	14201	GCTCCAAATGAATGCGATCAGACTTACCAACCAATGATGAAGATATTGATCTCTCCCC	14260
QY	275	IleIleAlaTyrSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal 294	
Db	14261	CTCATTTGCCCTGGAGCAAGGACATACCTGSCACAGTTTGAGATAAGACATTTCTTGGCAATC	14320

QY 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaAlaArgTyrSerTrpTrp 314
Db 14321 CTCCAATACCAGCATCTGTCTTCATGGGTCTGTATATTTTCGCCCGTGGTAGTGGCTC 14380
QY 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuLeuGlu 334
Db 14381 TTTTGGAGCTGGAGATATACCTCTACAGCAGTGTCTCACCTGTTCGACAGGTGTGGAG 14440
QY 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
Db 14441 AAGGGAACCTGTTCTGTTCACTACTTTTGGTTCGTCCGGACAGCGTGTATCTTCTCCT 14500
QY 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374
Db 14501 GGT---TGAAGCCATTAGTATGATGGCGGTGACTGAGCTCATGTCCGGCATGTGCTG 14557
QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGlnValTyrAsnGluSerLysAspPhe 394
Db 14558 GGCTTTGTATTGTTACTTAGCCACAATGGGATGGAGTTTATATTCGTTCTAAAGAATTC 14617
QY 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
Db 14618 GTGAGTGCACAGATCGTATCCACACGGGATATCAAGGAAACATATTCAACGACTGGTTC 14677
QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHisAsn 434
Db 14678 ACTGGTGGCCTTAACAGGCAATAGAGCAATCATCTTTCCCAACAATGCCAGGCATATT 14737
QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
Db 14738 TTAAACAAATAGCACCTAGAGTGGAGGTGTTCTGTGAAGAAACACGGTCTGTGTACGAA 14797
QY 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
Db 14798 GACGTATCTATTGCTACCGGCACCTTGCAAGGTTTGAAGAGCATTGAAGGAAGTCCGC-- 14854
QY 475 GluAlaSerIleArgLeuHisAla 482
Db 14855 GAGGCTGGGCAGAGCAGCATGCT 14878

RESULT 12
AAF25731
ID AAF25731 standard; DNA; 520 BP.
XX
AC AAF25731;
XX
DT 06-APR-2001 (first entry)
XX
DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 5.
XX
KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic; ds.
XX
OS Ceratodon purpureus.
XX
PN WO200075341-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-EP005274.
XX
PR 07-JUN-1999; 99DE-01025718.
XX
PR 22-DEC-1999; 99DE-01062409.
XX
PA (BADI) BASF AG.
XX
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringner U;
XX
DR WPI; 2001-112150/12.
DR P-PSDB; AAB46437.
XX
PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for

PT producing plant oils with increased content of unsaturated fatty acids.
XX
PS Example 6; Page 51; 69pp; German.
XX
CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
CC be used to suppress expression of (II), resulting in oils with increased
CC content of saturated fatty acids
XX
SQ Sequence 520 BP; 124 A; 116 C; 136 G; 144 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.97e-95 Length: 520
Score: 925.00 Matches: 172
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.42% Mismatches: 0
Query Match: 35.65% Indels: 0
DB: 4 Gaps: 0

US-09-980-468-2 (1-483) x AAF25731 (1-520)

QY 251 IleHisHisThrAlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIle 270
Db 2 ATTCATCATCTGCTCCGAATGAGTGGCAGCAAGTACACACTCTAGACGAAGACATT 61
QY 271 AspThrLeuProIleIleAlaTrpSerLysGluIleLeuProLeuPheMetAlaArg 290
Db 62 GATACTCTCCCATCATTTGCTGGAGCAAGGAAATTTGGCCACCCTTGAGAGCAAGAGA 121
QY 291 IleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeuProLeuPheMetAlaArg 310
Db 122 ATTTTGGAGTGTCTTCGATATCAGCACTACATGATTTCTGCTCTATTGTTTCATGGCCCG 181
QY 311 TyrSerTrpThrPheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrLys 330
Db 182 TACAGTTGGACTTTTGGAGTTTGTCTCTTCACATTCATCTGATTGAGCACCAGCAAG 241
QY 331 GlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPhe 350
Db 242 GGATTGATAGAGAAGGGAACAGTTGCTTTTCACTACGCTGGTTCAGTTGGGCTGCGTTC 301
QY 351 HisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAla 370
Db 302 CATATTTTCCCGGTGTCCGTAAGCCTCTTTCGCTGGATGGTAGCAACTGAGCTTGTGGCC 361
QY 371 GlyLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGlu 390
Db 362 GGTTTGTTGTTGAGTTCCTGTTTACGTTGAGTCACATGCAATGGAAGGAGGTTTACAATGAA 421
QY 391 SerLysAspPheValArgAlaGlnValIleThrThrArgAscThrLysArgGlyTrpPhe 410
Db 422 TCGAAGGACTTCTGTGAGAGCCAGGTTATTACCACCCGTAACACCAAGCGAGGCTGCTTC 481
QY 411 AsnAspTrpPheThrGlyLeuAspThrGlnIleGlu 423
Db 482 AACGATTGGTTCACTGGGGGACTCGACACCCAGATTGAG 520

RESULT 13
AAZ47129

ID AA247129 standard; DNA; 1374 BP.
XX AC AA247129;
XX DT 28-MAR-2000 (first entry)
XX DE Fungal delta6-desaturase coding sequence.
XX KW Polyunsaturated fatty acid; fungus; delta6-desaturase; animal feed;
XX KW transgenic animal; malnutrition; biosynthesis; ds.
XX OS Unidentified.
XX PN WO9961602-Al.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US012088.
XX PR 29-MAY-1998; 98US-00087578.
XX PA (OHIS) UNIV OHIO STATE.
XX PI Kopchick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;
XX DR WPI; 2000-072619/06.
XX DR P-PSDB; AAY56045.
XX PT Producing essential fatty acids and long-chain polyunsaturated fatty
XX acids, for use in nutritional, animal feed and medical formulations.
XX PS Disclosure; Fig 8; 7-pp; English.
XX CC The invention relates to a method of generating novel compositions
XX comprising animal cells producing essential fatty acids (FAs). The animal
XX cells are produced by transforming cells, e.g. embryonic stem cells, with
XX nucleic acid encoding heterologous enzymes involved in fatty acid, e.g.
XX long chain or polyunsaturated fatty acid (PFA) biosynthesis. This
XX sequence is an example of such a nucleic acid sequence and encodes a
XX fungal delta6-desaturase. The essential FAs obtained can be used in
XX nutritional formulations or animal feed formulations. The long chain PFAs
XX can be used in nutritional formulations, cosmetic formulations or animal
XX feed formulations. The products can also be used for producing transgenic
XX animals which can be used for producing essential FAs which can be used
XX for producing downstream products such as leukotrienes, thromboxanes,
XX arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid. The
XX products can also be used in cell culture. The animal or milk fat
XX produced can be administered to treat malnutrition
SQ Sequence 1374 BP; 257 A; 387 C; 378 G; 352 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.01e-85 Length: 1374
Score: 841.50 Matches: 177
Percent Similarity: 55.21% Conservative: 72
Best Local Similarity: 39.25% Mismatches: 159
Query Match: 32.43% Indels: 43
DB: 3 Gaps: 10

US-09-980-468-2 (1-483) x AA247129 (1-1374)
QY 62 ThrTyrSerLeuAlaAspVal-----AlaSerHisAspArg 73
Db 25 ACGTTTACTCGGCGCGAGGTTTGAATCCGAGGCTCTGAATGAGGGCAAGAGGATGCC 84
QY 74 ProGlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAsp 93
Db 85 GAGGCACCCCTTCTTGATGATCATCGACAACAAGGTGTACGATGTCCGCGAGTTCGTCCT 144
QY 94 AspHisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPhe 113
Db 145 GATCATCCCGGTGGAAGTGTGATTTCTCAGGCACGTTGGCAAGGACGGCACTGACGTC 204

QY 114 AlaThrPheHisProAlaAlaTyrLysGlnLeuAsnAspTyrTyrIleGlyAspLeu 133
Db 205 GACACTTTTCAACCCCGAGGCTGCTTGGGAGACTCTGCCAACTTTTACGTTGGTGATATT 264
QY 134 -----AlaArgGluGluProLeuAspGluLeuLeuLysAspTyrArgAspMetArg 150
Db 265 GACGAGAGCGACCGCATATCAAGAATGATGACTTGGCGCGAGGTCGCGAAGCTGCGT 324
QY 151 AlaGluPheValArgGluGlyLeuPheLysSerSerLysAlaTyrPheLeuLeuGlnThr 170
Db 325 ACCTTGTTCAGTCTCTTGGTTACTACGATTCTTCCAAGGCATACTACGCCCTTCAAGTTC 384
QY 171 LeuIleAsnAlaAlaLeuPheAlaAlaSerIleAlaThrIleCysTyr-----AspLys 188
Db 385 TCGTTCAACCTCTGCATCTGGGGTTTGTGACGGTCAATGTGGCCAAAGTGGGGCCAGACC 444
QY 189 SerTyrTrpAlaIleValLeuSerAlaSerLeuMetGlyLeuPheValGlnCysGly 208
Db 445 TCGACCCCTCGCCAAACGCTCTCGGCTGCGCTTTTGGGTCTGTTCTGGCAGCAGTGGGA 504
QY 209 TrpLeuAlaHisAspPheLeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhe 228
Db 505 TGGTTGGCTCAGCACTTTTGCATCACCAGGCTCTCCAGGACCGTTTCTGGGGTGATCTT 564
QY 229 PheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTyrTrpArgThrLys 248
Db 565 TTCGGCGCCTTCTTGGGAGGTCTCTGCCAGGCTTCTCGTCTCTGTTGGTGAAGGACAAG 624
QY 249 HisAsnIleHisThrAlaProAsnGluCysAspGluGlnTyrThrProLeuAspGlu 268
Db 625 CACAACACTCACCCAGCGCCGCCCAACGCTCCACGGCGAG-----GATCCC 669
QY 269 AspIleAspThrLeuProIleIleAlaTrpSerLys-----GluIleLeuAlaThr 285
Db 670 GACATTGACACCCACCCTCTGTGTGACCTGGAGTGAGATGGTGGAGATGTTCTCGGAT 729
QY 286 ValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeu----- 303
Db 730 GTCCCAAGATGAGGAGCTGACCCGCGCATG-----TGTGCGGCTTTCATGTTCTCTGA 783
QY 304 -----ProLeuLeuPheMetAlaArgTyrSerTyrPheGlySerLeu 318
Db 784 ACCTGGTTTACTTCCCATCTCTCGTTTGGCGGCTCTCTCTGTTGCTTCCAGTCCATT 843
QY 319 LeuPheThrPheAsnProAspLeuSerThrThrLys----- 330
Db 844 CTCTTTGTGCTG---CTTAACGGTCAGGCGCCACAAAGCCCTGGGCGCGGTGCCCAATC 900
QY 331 GlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTyrPheSerTyrAlaAlaPhe 350
Db 901 TCGTTGGTCGAGCAGCTGCGCTTGGATGACCTGGACCTGGTACCTCGCCACCATGTTTC 960
QY 351 HisIleLeuProGlyValAlaLysProLeuAlaTyrMetValAlaThrGluLeuValAla 370
Db 961 CTGTTTCATCAAGGATCCCGTCAACATGCTGGTGATCTTTTGGTGTGCGAGCGGTGTGC 1020
QY 371 GlyLeuLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGlu 390
Db 1021 GGAAACTTGTGTGGCGATCGTGTCTCGCTCAACCAACACCGTATGCTGTGATCTCGAAG 1080
QY 391 SerLys-----AspPheValArgAlaGlnValIleThrThrArgAsnThrLys 406
Db 1081 GAGGAGCGGTGCGATATGGATTTCTTCAAGAGCAGATCATCAGGTCGTGATGTCCAC 1140
QY 407 ArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThrGlnIleGluHisHisLeu 426
Db 1141 CCGGTCTATTGGCAACTGTTTACGGGTGGATTGAATATCATCATCGAGCACCACCTTG 1200
QY 427 PheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCys 446
Db 1201 TTCCCTTCGATGCTCGCCACAACTTTTCAAAGATCCAGCCTGCTGTCSAGACCCTGTGC 1260
QY 447 LysLysHisGlyLeuGluTyrAspAsnValSerValValGlyAlaSerValAlaValVal 466


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Db 1081 GAGGAGGGGTCGATGATGATTTCTTCACGAAGCAGATCATACGGGTCTGATGTCAC 1140
QY 407 ArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThrGlnIleGluHisLeu 426
Db 1141 CCGGGTCTATTGCGCAACTGGTTCACGGGTGGATTGAACATCATGATCGAGCACCATTG 1200
QY 427 PheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCys 446
Db 1201 TTCCCTCGATGCCTCGCCACACTTTTCAAGATCCAGCCTCTCTGTCGAGACCCTGTGC 1260
QY 447 LysLysHisGlyLeuGluTyrAspAsnValSerValValGlyAlaSerValAlaValVal 466
Db 1261 AAAAAGTACAAATGTCGATACCAACACCGGTATGATCGAGGAACTGCAGAGGTCTTT 1320
QY 467 LysAlaLeuLysGluIleAlaAspGluAlaSer 477
Db 1321 AGCCGTCTGAACGAGGTCTCCAGGTCCTCC 1353
```

```
RESULT 15
AAV63624
ID AAV63624 standard; cDNA; 1617 BP.
XX
AC AAV63624;
XX
DT 15-FEB-1999 (first entry)
XX
DE cDNA encoding a delta-6 desaturase enzyme.
XX
KW fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition;
KW inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes;
KW eczema; platelet aggregation; vasodilation; cholesterol level;
KW endometriosis; premenstrual syndrome; myalgic encephalomyelitis;
KW chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome;
KW hypertension; inflammatory skin disorder; ss.
XX
OS Mortierella alpina.
```

```
XX Location/Qualifiers
FH 71..1444
PT CDS
PT /*tag= a
PT /product= "delta-6 desaturase"
XX
PN WO9846763-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-US007126.
XX
PR 11-APR-1997; 97US-00834655.
XX
PA (CALJ ) CALGENE LLC.
PA (ABBO ) ABBOTT LAB.
XX
PI Knutson D, Mukerji P, Huang Y, Thurmond J, Chaudhary S;
PI Leonard AE;
XX
PI WPI; 1998-594582/50.
PI P-PSDB; AAW84137.
XX
PT New isolated fatty acid desaturase enzymes - used for the production of
PT polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions,
PT nutritional compositions, cosmetics or animal feed.
XX
PS Claim 1; Fig 3A-E; 165pp; English.
```

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XX The present sequence encodes a Mortierella alpina fatty acid delta-6
CC desaturase enzyme. The enzyme sequence is used in the methods of the
CC invention. The specification describes methods for desaturating a fatty
CC acid and for producing a desaturated fatty acid by expressing increased
CC levels of a desaturase. The present desaturase is an enzyme which
CC introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty
CC acid molecule. The enzyme can be used for desaturating fatty acids. The
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CC enzyme can be used to produce polyunsaturated fatty acids, which can be
CC used for treating malnutrition, in pharmaceutical compositions, in
CC cosmetics or in animal feed. The polyunsaturated fatty acids can be used
CC for treating e.g. restenosis after angioplasty, inflammation, rheumatoid
CC arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood
CC pressure. They can also be used to inhibit platelet aggregation, cause
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
CC wall smooth muscle and fibrous tissue, reduce or prevent gastro-
CC intestinal bleeding and other side effects caused by non-steroidal anti-
CC inflammatory drugs, prevent or treat endometriosis and premenstrual
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral
CC infections, treat AIDS, multiple sclerosis, acute respiratory syndrome,
CC hypertension and inflammatory skin disorders
```

SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 U; 0 Other;

Alignment Scores: 5.13e-85 Length: 1617
Pred. No.: 841.50 Matches: 177
Score: 55.21% Conservative: 72
Best Local Similarity: 39.25% Mismatches: 159
Query Match: 32.43% Indels: 43
DB: 2 Gaps: 10

US-09-980-468-2 (1-483) x AAV63624 (1-1617)

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QY 62 ThrTyrSerLeuAlaAspVal-----AlaSerHisAspArg 73
Db 95 ACCTTACTCGGGCCGAGGTTTGAATCCCGAGGCTCTGAATGAGGCAAGAGGATGCC 154
QY 74 ProGlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAsp 93
Db 155 GAGGACCCCTTCTTGAATGATCATCGACAAAGGTGTACGATGTCCCGAGTTCGTCCT 214
QY 94 AspHisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPhe 113
Db 215 GATCATCCCGGTGGAAGTGTGATTCTCAGCACGCTTGGCAAGGACGCGACTGACGCTTT 274
QY 114 AlaThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrTyrIleGlyAspLeu 133
Db 275 GACACTTTTACCCCGAGGCTGTCTGGAGACTCTTGGCAACTTTTACGTTGGTGATATT 334
QY 134 -----AlaArgGluGluProLeuAspGluLeuLeuLysAspTyrArgAspMetArg 150
Db 335 GACGAGAGCGACCGGATATCAAGATGATGACTTTGCGGCCGAGGTCCGCAAGCTGCGT 394
QY 151 AlaGluPheValArgGluGlyLeuPheLysSerSerLysAlaTrpPheLeuLeuGlnThr 170
Db 395 ACCTTGTTCCAGTCTCTTGGTTACTACGATTCTTCCAAGGCATACCTACGCTTCAAGGTC 454
QY 171 LeuIleAsnAlaAlaLeuPheAlaAlaSerIleAlaThrIleCysTyr-----AspLys 188
Db 455 TCGTTCAACCTCTGCATCTGGGGTTTGTGACCGGTCTTGTGGCCAGTGGGCCAGACC 514
QY 189 SerTyrTrpAlaIleValLeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGly 208
Db 515 TCGACCTTCGCCAACGTTGCTCTCGGCTGCGCTTTTGGGTCTGTTCTGGCAGCAGTGGGA 574
QY 209 TrpLeuAlaHisAspPheLeuHisGlnValPheGluAsnArgThrAlaAsnSerPhe 228
Db 575 TGGTTGGCTCAGCACTTTTGTGATCACCAGGTCTTCCAGGACCGTTTCTGGGGTGATCTT 634
QY 229 PheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTrpArgThrLys 248
Db 635 TCGGGCGCTTCTTGGAGGTGTCTGCCAGGCTTCTCGTCTCTGTTGGTGAAGGACAAG 694
QY 249 HisAsnIleHisThrAlaProAsnGluCysAspGluGlnTyrThrProLeuAspGlu 268
Db 695 CACAACACTCACACGCGCGCCGCCAACGTCACGGCGAG-----GATCCC 739
QY 269 AspIleAspThrLeuProIleIleAlaTrpSerLys-----GluIleLeuAlaThr 285
Db 740 GACATTGACACCCACCTCTGTTGACCTGGAGTGCATGCGTTGGAGATGTTCTCGGAT 799
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QY	286	ValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeu-----	303
DB	800	GTCCCGATGAGGAGCTGACCCGCATG-----TGCTCGCTTTTCATGGTCTCTGAACCAAG	853
QY	304	-----ProLeuLeuPheMetAlaArgTyrSerTirPThrPheGlySerLeu	318
DB	854	ACCTGGTTTACTTCCCATCTCTCGTTTGCCCGTCTCTCTGGTGCCTCCAGTCCATT	913
QY	319	LeuPheThrPheAsnProAspLeuSerThrThrLys-----	330
DB	914	CTCTTTGTCTG---CCTAACGGTCAAGCCCAACAGCCCTCGGGCGCGGTGTGCCCATC	970
QY	331	GlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTirPheSerTirPAlaAlaPhe	350
DB	971	TCGTTGGTCGAGCAGCTGTGGCTTGCGATGCACCTGGACCTGGTACCTCGCCACCATGTTT	1030
QY	351	HisIleLeuProGlyValAlaLysProLeuAlaTirPMetValAlaThrGluLeuValAla	370
DB	1031	CTGTTTCATCAAGGATCCCGTCAACATGCTGGTGTACTTTTGGTGTGCGACGGCGGTGTC	1090
QY	371	GlyLeuLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGlu	390
DB	1091	GGAAACTTGTGGCGATCGTGTCTCGCTCAACCACACGGTATGCCCTGTGATCTCGAAG	1150
QY	391	SerLys-----AspPheValArgAlaGlnValIleThrThrArgAsnThrLys	406
DB	1151	GAGGAGCGGTGATATGGATTTCTTCAGAACGACATCATCACGGTCTGTATGTCCAC	1210
QY	407	ArgGlyTirPheAsnAspTirPheThrGlyGlyLeuAspThrGlnIleGluHisHisLeu	426
DB	1211	CCGGGTCTATTTCGCACTGGTTACGGGTGGATTGAACACTATCAGATCGAGCACCACATTG	1270
QY	427	PheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCys	446
DB	1271	TTCCTCTCGATGCTCGCCACAACCTTTCAAAGATCGAGCCTGTGTCTGAGACCCCTGTGC	1330
QY	447	LysLysHisGlyLeuGluTyrAspAsnValSerValValGlyAlaSerValAlaValVal	466
DB	1331	AAAAAGTACAATGTCCGATACCACACCACCGGTATGATCGAGGGAACCTGCAGAGGTCTTT	1390
QY	467	LysAlaLeuLysGluIleAlaAspGluAlaSer	477
DB	1391	AGCCGTCTGAACGAGGTCTCCAAGGCTGCCTCC	1423

Search completed: June 19, 2004, 03:06:48
Job time : 689 secs

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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:00:51 ; Search time 18 Seconds
(without alignments)
1397.216 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTDFLFLGLTWSKYSV.....AVWKALKEIADERSIRLHAH 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 3.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	500.5	19.3	444	1 FADS_BRARE	Q9dex7 brachydanio
2	200	7.7	359	1 LLCN_SYN3	Q08871 synechocyst
3	193.5	7.5	132	1 CYB5_BORCF	O04354 borago offi
4	190.5	7.3	137	1 CYB5_ORYSA	P49100 oryza sativ
5	179.5	6.9	136	1 CYB5_TOBAC	P49038 nicotiana t
6	172.5	6.6	135	1 CYB5_CUSRE	P49037 cuscutoa ref
7	172	6.6	135	1 CYB5_TOBAC	P49039 nicotiana t
8	170.5	6.6	134	1 CY52_ARATH	O48845 arabidopsis
9	166.5	6.4	900	1 NIA_IOTJA	P39869 lotus japon
10	164	6.3	918	1 NIA_CUCMA	P17569 cucurbita m
11	162.5	6.3	435	1 FD3D_ARATH	P48622 arabidopsis
12	160.5	6.2	864	1 NIA_VOLCA	P36841 volvox cart
13	160	6.2	120	1 CYB5_YEAST	P40312 saccharomyc
14	160	6.2	890	1 NIA2_PHAVU	P39866 phaseolus v
15	159.5	6.1	380	1 FD3E_PHAU	P32291 phaseolus a
16	158.5	6.1	460	1 FD3C_RICCO	P48619 ricinus com
17	157	6.1	124	1 CY51_SCHPO	O94391 schizosacch
18	157	6.1	890	1 NIA2_SOYBN	P39870 glycine max
19	154.5	6.0	318	1 NIA2_CHLVU	Q01170 chlorella v
20	154	5.9	414	1 CYBR_DROME	P19967 drosophila
21	154	5.9	591	1 CYB2_YEAST	P00175 saccharomyc
22	154	5.9	886	1 NIA1_SOYBN	P54233 glycine max
23	153.5	5.9	134	1 CY51_ARATH	Q42342 arabidopsis
24	153	5.9	917	1 NIA1_ARATH	P11832 arabidopsis
25	153	5.9	917	1 NIA2_ARATH	P11035 arabidopsis
26	150	5.8	134	1 CYB5_BRAOL	P40934 brassica ol
27	150	5.8	911	1 NIA1_BRANA	P39867 brassica na
28	149	5.7	881	1 NIA1_PHAVU	P39865 phaseolus v
29	149	5.7	904	1 NIA2_TOBAC	P08509 nicotiana t
30	149	5.7	911	1 NIA2_BRANA	P39868 brassica na
31	148.5	5.7	146	1 CYM5_RAT	P04166 rattus norv
32	148.5	5.7	453	1 FD3C_SOYBN	P48621 glycine max
33	148	5.7	384	1 SCS7_YEAST	Q03529 saccharomyc

34	147.5	5.7	902	1 NIA_PHYIN	P39864 phytophthor
35	147	5.7	131	1 CYB5_RHIST	Q9hfv1 rhizopus st
36	146.5	5.6	380	1 FD3E_SOYBN	P48625 glycine max
37	146.5	5.6	386	1 FD3E_ARATH	P48623 arabidopsis
38	143.5	5.5	926	1 NIA_SPIOL	P23312 spinacia ol
39	143	5.5	443	1 FD6C_BRANA	P48627 brassica na
40	142	5.5	129	1 CY52_SCHPO	Q9usm6 schizosacch
41	142	5.5	911	1 NIA_LYCES	P17570 lycopersico
42	141.5	5.5	379	1 FD3E_TOBAC	P48626 nicotiana t
43	141	5.4	383	1 FD62_SOYBN	P48631 glycine max
44	141	5.4	898	1 NIA_BETVE	P27783 betula verr
45	141	5.4	909	1 NIA_PETHY	P36859 petunia hyb

ALIGNMENTS

RESULT 1
FADS_BRARE
ID FADS_BRARE STANDARD; PRT; 444 AA.
AC Q9DEX7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-).
GN FADS2 OR FADSD6.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21592990; PubMed=11724940;
RA Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,
Sargent J.R., Teale A.J.;
RT "A vertebrate fatty acid desaturase with delta5 and delta6
activities.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).
CC -!- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6
activities. May represent a component of the polyunsaturated fatty
acid biosynthesis pathway.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SIMILARITY: Belongs to the fatty acid desaturase family.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF309556; AAG25710.1; -.
DR HSSP; P00173; 1JEX.
DR ZFIN; ZDB-GENE-011212-1; fads2.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme 1; 1.
DR PRINTS; PR00363; CYTOCHROME B5.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS00191; CYTOCHROME_B5_1; FALSE_NEG.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Fatty acid biosynthesis; Oxidoreductase; Heme.
FT DOMAIN 18 95 HEME-BINDING.
FT METAL 53 53 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 76 76 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 444 AA; 52032 MW; 6AA25A1DC1DC0F65 CRC64;

	Query Match	19.3%;	Score 500.5;	DB 1;	Length 444;
	Best Local Similarity	28.8%;	Pred. No. 1.5e-34;		
	Matches 130;	Conservative 78;	Mismatches 164;	Indels 79;	Gaps 16
QY	62	TYSLADVASHDRPGDCWMIWKEKVDISRFADDHPGG-TVISTYFGRDGTDFATFHP--	118		
DB	20	SYTWEVQKTKHGQWVVERKVINVSQWVKRHPGGLRIILGHYAGEDATEAFTAFHPNL	79		
QY	119	PAAWKQLNDYYIGDLAREEPLDE-----LLKDYRDMRAEFVREGLFKSSKAWFLLOTLI	172		
DB	80	QLVRKYLKPELLIGELEASEPSQDRQKNAALVEDFRALRERLEAEGCFKQPLFFALHLGH	139		
QY	173	KAALFAAS-ATICYDKSYWA-IVLSASLMGLFVQCCGWLAEHFLKQOVFNERTANSFFGY	231		
DB	140	ILLLEAIAFMVWYFGTGWINTLIVAVILATAQSQAGWLQHDFGHLSVPKTSGMNHLVHK	199		
QY	232	LFGNCVLGFSVSWWRTKHNTHHTAPNECDEQYTPLEDIDITLPIAWSKEILATVE----	287		
DB	200	FVIGHLKGASAGWNNHRHFQHHAKENIFKX-----DFDVNML-----NAFVVGNVQPVVEY	249		
QY	288	SKRILRLVLOYQHYMILPLLEFMARYSWTFGSLFLTENPDLSSTTKGLIEKGTVAFYHAFPSW	347		
DB	250	GVKKIKHLPYNH-----QHKY-----FFFIGPPL-----LIP-----VYFQF	281		
QY	348	AAFH--ILPGVAKPLAWMVA-----TELV-----AGLLLG-----VFTLS	381		
DB	282	QIFHNMI SHGMWVDLLWCISYYVRYELCYTFQYGVFWAIILFNFRFMESHFWVWTQMS	341		
QY	382	HNGKEV-YNESKOFVRAQVITTRNTKRGWFENDWFTGGLDTOIEHHLFPTVPRHNYPKIAP	440		
DB	342	HIPMNIDYEKNQDWLSMQLWATCNIEQSAFNDFWFSGHLNFQIEHHLFPTVPRHNYWRAAP	401		
QY	441	QVEALCKKHGLEVDNSVVGASVAVVVKALKE	471		
DB	402	RVRALCEKYGKVGXOEKTLYGAFADIIIRSLK	432		

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RESULT 2
LLCD_SYNY3          STANDARD;      PRT;    359 AA.
ID _LLCD SYNY3
AC Q08871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Linoleoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
GN DES6 OR SLL0262.
OS Synechocystis sp. {strain PCC 6803}.
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93283633; PubMed=8389613;
RA Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
RT "Isolation of a delta 6-desaturase gene from the cyanobacterium
RT Synechocystis sp. strain PCC 6803 by gain-of-function expression in
RT Anabaena sp. strain PCC 7120.";
RL Plant Mol. Biol. 22:293-300(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiratsawa M., Sugihara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- CATALYTIC ACTIVITY: Linoleoyl-CoA + AH(2) + O(2) = gamma-
CC linolenoyl-CoA + A + 2 H(2)O.
CC -!- COFACTOR: Iron.
```

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EMBL; L11421; AAA27286.1; --
EMBL; D90914; BAA18502.1; --
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
KW Oxidoreductase; Iron; Complete proteome.
SQ SEQUENCE 359 AA; 41425 MW; 33FB165AEB98C05F CRC64;

Query Match 7.7%; Score 200; DB 1; Length 359;
Best Local Similarity 24.0%; Pred. No. 2.6e-09;
Matches 86; Conservative 50; Mismatches 141; Indels 82; Gaps 17.

QY 151 AEFVREGLPKSSKAWFLQLTLLNAA-LFAASLATICYDKSYAWIVLSA-----SLMGLF 203
| | | | | : | | | | | : | | | | | : | | | | | : | |
Db 25 AYFAEHLGTQRDNPSMYLKTLLIIVLWLSA-----WAFVLPAPVTFPVRLLGCM 73
| | | | | : | | | | | : | | | | | : | | | | | : | |
QY 204 VQCGWLA-----HDFLHQQVFENRTANSFQYLPFGNCVLGFSVSWWRTKHN-IHHTAP 256
| | | | | : | | | | | : | | | | | : | | | | | : | |
Db 74 VLAIALAAPSFNVGHDANHNAYSSNPHINRVLGMYTD--FVGLSSFLWRRYRHNVLHHTYT 131
| | | | | : | | | | | : | | | | | : | | | | | : | |
QY 257 NECDEQYPLDEDIDTLPIAWSKEILATVESKRILRVLQYQHMYMLPLLFEMARYSWTFG 316
| | | | | : | | | | | : | | | | | : | | | | | : | |
Db 132 N-----ILGHDVE---IHGDGAVRMSPEQEHV-GIYRFQQFYIWGLYLFIPFYW--- 176
| | | | | : | | | | | : | | | | | : | | | | | : | |
QY 317 SLLFTFNPDLSTKG-----LIEKGTVAHYAWFSWA-AFHILPGVAKP--LA 361
| | | | | : | | | | | : | | | | | : | | | | | : | |
Db 177 ---FLYDVYLVLNKGKYHDHKIPFPQPLESLASLLGIKLLWLGYYVGLPLALGFSIPEVLI 233
| | | | | : | | | | | : | | | | | : | | | | | : | |
QY 362 MMVATELVAGLLGFVPTLSHNGKEVYNESKDFVR-----AQVITRN--T 405
| | | | | : | | | | | : | | | | | : | | | | | : | |
Db 234 GASVTYMTYGIIVCVTIFMLAH-----VLESTFELTPDGESGAIDDEWAICQRTTANFAT 288
| | | | | : | | | | | : | | | | | : | | | | | : | |
QY 406 KRGWENDWFTGLDTQIEHHLFPTMPRENYPKIAPQVEALCKHGLEYDNVSVVGASVA 464
| | | | | : | | | | | : | | | | | : | | | | | : | |
Db 289 NNPFWN-WFCGGLNHQVTHLFPNICHYHYPQLENIKDVCEFGVEYKVYPTFKAAIA 346
| | | | | : | | | | | : | | | | | : | | | | | : | |

RESULT 3
CYB5_BOROF STANDARD; PRT; 132 AA.
AC O04354;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
CS Borago officinalis (Bourrache) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Boraginaceae; Borago.
OX NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268723; PubMed=9108131;
RA Sayanova O., Smith M.A., Lapinskas P.A., Stobart K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216 (1997).
CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By similarity).
CC -!- SUBCELLULAR LOCATION: Microsomal membrane. Bound to the
CC cytoplasmic side of the endoplasmic reticulum (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b5 family.


```
DR PIR; S49200; S49200.
DR HSSP; P04166; IB5M.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR Electron transport; Transmembrane; Heme; Iron; Microsome;
KW Multigene family.
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 135 AA; 14869 MW; A36CCA081A72ECBC CRC64;

Query Match 6.6%; Score 172; DB 1; Length 135;
Best Local Similarity 41.1%; Pred. No. 1.8e-07;
Matches 30; Conservative 21; Mismatches 20; Indels 2; Gaps 2;

QY 63 YSLADVASHDRPGDCWMIVKEKVDISRFDADHP-GGTVISYFGRDGTDFVATF-HPPA 120
Db 8 FTAEVSNHNNNAKDWLIISGKYNVNTKFLDHPGCGEVLLSATGKDADDDFEDIGHSS 67

QY 121 AWKQLNDYYIGDL 133
Db 68 ARAMLEYYVVDI 80

RESULT 8
CY52_ARATH STANDARD; PRT; 134 AA.
AC O48845;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cytochrome b5 isoform 2.
GN ATG32720 OR F24L7.14.
OS Arabidopsis thaliana (Mouse-ear cress).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronging C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial membrane. Bound to the
CC cytoplasmic side of the endoplasmic reticulum (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b5 family.
CC
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CC
CC EMBL; AC003974; AAC04491.1; -.
DR PIR; T00796; T00796.
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DR HSSP; P04166; IB5M.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR Electron transport; Transmembrane; Heme; Iron; Microsome;
KW Multigene family.
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 134 AA; 15016 MW; B405F5430F5716C1 CRC64;

Query Match 6.6%; Score 170.5; DB 1; Length 134;
Best Local Similarity 28.8%; Pred. No. 2.3e-07;
Matches 40; Conservative 36; Mismatches 38; Indels 25; Gaps 7;

QY 63 YSLADVASHDRPGDCWMIVKEKVDISRFDADHPGG-TVISYFGRDGTDFVATF-HPPA 120
Db 8 FTLSEVSEHNQAHDCWIVNGKYNVNTKFLDHPGDDVLLSSTGKDADDDFEDVGHSES 67

QY 121 AWKQLNDYYIGDLAREEP--LDELLK-----DY-RDMRAEFVREGLEKSSKAWFLLOT 170
Db 68 AREMMEQYIVGEI---DPTTPKKVKYTPFKQPHYNQDKTSEFIK-----LLQF 114

QY 171 LINAALFAASIATICYDKS 189
Db 115 LVPLAILGLAVGIRIYTKS 133

RESULT 9
NIA_LOTJA STANDARD; PRT; 900 AA.
AC P39869;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
GN NIA.
OS Lotus japonicus.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
CC eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
CX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Gifu / B-129;
RA Waterhouse R.N., Smyth A.J., Prosser I.M., Forde B.G., Clarkson D.T.;
RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Requires FAD, a heme group (called cytochrome b-557) and
CC one molybdenum atom.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X80670; CAA56696.1; -.
DR PIR; S47029; S47029.
DR HSSP; P17571; 2CND.
```


RESULT 12
FD3D ARATH STANDARD; PRT; 435 AA.
AC P48622;
CT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Temperature-sensitive omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
GN FAD8 OR AT5G05580 OR NCPI0.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Aerial parts;
RX MEDLINE=95148742; PubMed=7846164;
RA Gibson S., Aronold V., Iba K., Somerville C.R.;
RT "Cloning of a temperature-regulated gene encoding a chloroplast omega-3 desaturase from Arabidopsis thaliana.";
RL Plant Physiol. 106:1615-1621(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;
RA Watahiki M.C., Yamamoto K.T.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned P1 clones.";
RL DNA Res. 4:215-230(1997).
CC -!- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactolipids, sulfolipids and phosphatidylglycerol.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -!- INDUCTION: BY LOW TEMPERATURE.
CC -!- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
CC -!- SIMILARITY: Belongs to the fatty acid desaturase family.
CC -----
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CC -----
DR EMBL; L27158; AAA65621.1; -.
DR EMBL; U08216; AAB60302.1; -.
DR EMBL; D17578; BAA04504.1; -.
DR EMBL; AB005241; BAB11547.1; -.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF03487; FA_desatase; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 435 TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE.
FT DOMAIN 156 160 HISTIDINE BOX-1.

FT DOMAIN 192 196 HISTIDINE BOX-2.
FT DOMAIN 359 363 HISTIDINE BOX-3.
SQ SEQUENCE 435 AA; 50136 MW; 3D77A8035A6214E1 CRC64;

Query Match 6.3%; Score 162.5; DB 1; Length 435;
Best Local Similarity 20.4%; Pred. No. 4.9e-06;
Matches 105; Conservative 66; Mismatches 180; Indels 163; Gaps 25;

QY 18 YSVYTHSYAGNYGPTLK-----HAKKVSAGKTAGQTLRQSVQD 57
DB 18 YPKHTTSFASNPKEPKFPNPKPPSSLLNSRYGFSKTRNWNALNVATPLTTLQSPSEED 77

QY 58 KK-----PGTYSLADVASHDRPGDCWMIWKEKVVYDISRFADHPGGTVISTYFGRDGT 111
DB 78 TEREDPGAPPPFNADIRA-AIPKHCW--VKNPWMSMSYVVRD-----VAIVFGL-AA 126

QY 112 VFATFHPPAAWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFVREGLFKSSKAWFLQL 171
DB 127 VAAFFNNWLLW-----PL-----YWFAGQTM 147

QY 172 INAALFAASIATICYDKSYWAIVLSASLMGLFVQCCWLAHDELHQOVFENRTANSFPGY 231
DB 148 -----FWA-----LFV-----LGHDCGHGFSNDPRLNSVACH 175

QY 232 LFGNCVLGFSVSWRTKHNHHTAPN--ECDEQYTPDELDEIDTLPPIAWSKEILATVESK 289
DB 176 LLHSSIL-VPYHGWEISRTHRHQNHGHVENDSHHELPEI-----YKNLEKTTQ-- 224

QY 290 RILRVLYQHYMILPFLFMARYSW--TFGSLLETFMPDLSTTKGLIEKGTVAHFYAWFSW 347
DB 225 -----MFRFTLPFPMLAYPFYLNRSRPGKQSGSHYHPSDLFLPKEKKOVLSTACWTAM 278

QY 348 AAFHI-LPGVAKPLA-----WMVATELVAGLLIGFVFTLSHNGKE-----VYNESK 392
DB 279 AALLVCINFMVGMPIQMLKLYGIPYWIFV-----MWLDFTYLLHHGHGDKLPWYRGKEW 332

QY 393 DFVRAQVITTRNTKRGWFDWFTGGLDTQIEHLLFTMPRHNYPKIAPOVEALCKKHGLE 452
DB 333 SYLRGG-LTTLD RDYGWINN-IHHDIGTHVIHLEFPQIPHHLVEATEAAKPVLGKYRE 390

QY 453 YDN-----VSVVGASVAVVKALKE---IADEASI 478
DB 391 PKNSGPLPLHLG---SLIKSMKQDHFVSDTG DV 421

RESULT 12
NIA_VOLCA STANDARD; PRT; 864 AA.
AC P36841;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
GN NITA.
OS Volvox carteri.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Volvocaceae; Volvox.
OX NCBI_TaxID=3067;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=f. Nagariensis / HK10;
RX MEDLINE=93013022; PubMed=1398126;
RA Gruber H., Goetinck S.D., Kirk D.L., Schmitt R.;
RT "The nitrate reductase-encoding gene of Volvox carteri: map location, sequence and induction kinetics.";
RL Gene 120:75-83(1992).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD, heme iron, and molybdenum-pterin as prosthetic groups. The heme group is called cytochrome b-557.
CC -!- SUBUNIT: Homodimer (by similarity).

CC -!- INDUCTION: By nitrate.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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DR EMBL; X64136; CAA45497.1; -.
DR PIR; JCL1422; JCL1422.
DR HSSP; P04166; 1B5M.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR001834; Cyt B5 reductase.
DR InterPro; IPR008335; Euk Mb_oxred.
DR InterPro; IPR008333; FAD_binding_6.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR005066; Mo-co dimer.
DR InterPro; IPR000572; Oxidored molyb.
DR InterPro; IPR001433; Oxred FAD/NAD(P).
DR Pfam; PF03970; FAD_binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; oxidored molyb; 1.
DR PRINTS; PR00406; CYTB5REDTASE.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRINTS; PR00407; EUMCPTERIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PDC00612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation.
FT METAL 139 139 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 193 193 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 376 376 INTERCHAIN (POTENTIAL).
FT METAL 532 532 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 555 555 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 864 AA; 96402 MW; 499529652CDD1C7 CRC64;

Query Match 6.2%; Score 160.5; DB 1; Length 864;
Best Local Similarity 40.0%; Pred. No. 1.7e-05;
Matches 32; Conservative 11; Mismatches 36; Indels 1; Gaps 1;
QY 60 PGTYSLADVASHDRPGDCWMIVKEKVDISRFDHPGGT-VISTYFGRDGTDFATFHP 118
Db 497 PROYTMEEVAHNTEESCWFVHGKVIDATPYLDHPGGAESILIVAGADATDFNSIHS 556
QY 119 PAAWKQLNDYYIGDLAREEP 138
Db 557 SKAKAMLAQYYIGDLVASKP 576

RESULT 13
CYB5_YEAST STANDARD; PRT; 120 AA.
ID CYB5_YEAST
AC P40312;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
GN CYB5 OR YNL111C OR N1949.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 28383 / FL100;
RX MEDLINE=94237477; PubMed=8181746;
RA Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.;
RT "Cloning and characterization of a yeast cytochrome b5-encoding gene
RT which suppresses ketoconazole hypersensitivity in a NADPH-P-450
RT reductase-deficient strain."
RL Gene 142:123-127(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97245296; PubMed=9090055;
RA de Antoni A., D'Angelo M., Dai Pero F., Sartorello F., Pandolfo D.,
RA Pallavicini A., Lanfranchi G., Valle G.;
RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
RT Saccharomyces cerevisiae reveals an unusually high number of
RT overlapping open reading frames."
RL Yeast 13:261-266(1997).
CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases. It plays a role in
CC fatty-acid desaturation and is also involved in several steps of
CC the sterol biosynthesis pathway, particularly in the 4-
CC demethylation of the 4,4'-dimethyl zymosterol.
CC -!- SUBCELLULAR LOCATION: Microsomal membrane. Bound to the
CC cytoplasmic side of the endoplasmic reticulum (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b5 family.
CC -----

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; L22494; AAA67468.1; -.
DR EMBL; Z69382; CAA93396.1; -.
DR EMBL; Z71387; CAA95990.1; -.
DR PIR; S63052; S63052.
DR HSSP; P04166; 1EUE.
DR GerMOnline; 143117; -.
DR SGD; S0005055; CYB5.
DR GO; GO:0005792; C:mitochondrion; IDA.
DR GO; GO:0016126; P:sterol biosynthesis; IDA.
DR InterPro; IPR001199; Cyt B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PDC00612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Iron; Microsome.
FT TRANSMEM 98 118 POTENTIAL.
FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 17 17 E -> Q (IN REF. 1).
SQ SEQUENCE 120 AA; 13297 MW; 598EF2A6730CAD19 CRC64;

Query Match 6.2%; Score 160; DB 1; Length 120;
Best Local Similarity 42.1%; Pred. No. 1.6e-06;
Matches 32; Conservative 14; Mismatches 28; Indels 2; Gaps 2;

QY 60 PGTYSLADVASHDRPGDCWMIVKEKVDISRFDHPGGT-TVISTYFGRDGTDFATF-H 117
Db 2 PKVYSYQEVAAHNGSPENFWIIIDKVDVVSQFKDHPGGDEIIMDLGGQDQATSFVDIGH 61
QY 118 PPAAWKQLNDYYIGDL 133
Db 62 SDEALRLIKGLYIGDV 77

RESULT 14

```
NIA2 PHAVU
ID NIA2 PHAVU STANDARD; PRT; 890 AA.
AC P39866;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR-2).
GN NIA2 OR NR2.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Saxa;
RA Jensen P.E., Hoff T., Stummann S.M., Henningsen K.W.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Requires FAD, a heme group (called cytochrome b-557) and
CC one molybdenum atom.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U01029; AAA95940.1; -.
CC PIR; T11805; T11805.
CC HSSP; P17571; 2CND.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008335; Euk_Mb_oxred.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001709; FPN_cyt_redctse.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR000572; Oxidored_molyb.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF00970; FAD_binding_6; 1.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-co_dimer; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC Pfam; PF00174; oxidored_molyb; 1.
CC PRINTS; PR00406; CYTB5RDTASE.
CC PRINTS; PR00363; CYTOCHROME_B5.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRINTS; PR00371; FNCR.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS00255; CYTOCHROME_B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT METAL 165 165 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 219 219 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 404 404 INTERCHAIN (POTENTIAL).
FT METAL 548 548 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 571 571 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 890 AA; 99995 MW; FC33B96F0139DE1E CRC64;

Best Local Similarity 30.3%; Pred. No. 2e-05;
Matches 46; Conservative 21; Mismatches 61; Indels 24; Gaps 6;

QY 3 LVTDFLNFLTWSKYSVYTH---SYAGNYGPTLKHAKVSAQ--GKTAGQTLRQSVQD 57
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 439 LIWNLMGMNNCW--FRVKNVCKPHKGEIGIVFEHPTQPGNPGGWMMAKXHLQCS-QE 495
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 KKPG-----TYSLADVASHDRPGDCWMIKVKVYDISRFADDPGGT-VI 101
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 496 AKPSLKSVSTPFMTASKMFSVSEVKHSSPDSAWIIVHGHVYDCTRFKLDHPGGTDSI 555
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 102 STYFGRDGTDFEATFFHPPAAWKQLNDYYIGDL 133
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 556 LINAGTCTEEFDAIHSDKAKKMLEDYRIGEL 587

RESULT 15
ID FD3E PHAAU STANDARD; PRT; 380 AA.
AC P32291;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)
DE (Indole-3-acetic acid induced protein ARG1).
GN ARG1.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypocotyl;
RA Yamamoto K.T., Mori H., Imaseki H.;
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
RT elongating hypocotyls of mung bean (Vigna radiata).";
RL Plant Cell Physiol. 33:13-20(1992).
CC -!- FUNCTION: Microsomal (ER) omega-3 fatty acid desaturase introduces
CC the third double bond in the biosynthesis of 18:3 fatty acids,
CC important constituents of plant membranes. It is thought to use
CC cytochrome b5 as an electron donor and to act on fatty acids
CC esterified to phosphatidylcholine and, possibly, other
CC phospholipids.
CC -!- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -!- INDUCTION: By auxin, ethylene and wounding.
CC -!- DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -!- SIMILARITY: Belongs to the fatty acid desaturase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D14410; BAA03306.1; -.
CC PIR; T10898; T10898.
CC InterPro; IPR005804; FA_desat_fam.
CC Pfam; PF00487; FA_desaturase; 1.
CC ProDom; PD001081; FA_desat_fam; 2.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 59 78 POTENTIAL.
FT TRANSMEM 208 231 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE_BOX-1.
FT DOMAIN 133 137 HISTIDINE_BOX-2.
FT DOMAIN 300 304 HISTIDINE_BOX-3.
SQ SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE16B CRC64;

Query Match 6.2%; Score 160; DB 1; Length 890;
```

Query Match		6.1%;	Score 159.5;	DB 1;	Length 380;
Best Local Similarity		23.0%;	Pred. No. 7.4e-06;		
Matches	77;	Conservative	48;	Mismatches	137;
				Indels	73;
				Gaps	16;
Qy	148	DNPAEFFVREGLFKS---	SKAWELLQTLINAALFAAS	IATICVDKSYWAI	VLAS---LMG 201
Db	34	DIRAAIPKHCWEKSTLRSLSY	VLRDVLVVTALAASAIS	FSW--FFWPLYWPAQGT	MFWA 91
Qy	202	LFVQCCGWLADFLHQOVFEN	TANSFFGYLFGNCVLF	GFSVSWRTKHN	IHTAPN--EC 259
Db	92	LFV-----LGHDCGHGSF	SNSSKLN	SVGHILHSLIL-V	PYNGWRI
Qy	260	DEQYTPLDDEDITLPIIAW	SKELATVESKRILRV	LQYQHYMILP	LLEMARYSW--TFGS 317
Db	146	DESWVPLTE-----	KVYKNLDD--MTR	MLRYS--FPP	PIFAYPPFYLWNRSPGX 189
Qy	318	LLFTFNPDLS	TTKGLIEKGTVA	FHYAFWSWA	AFHILPGVAKPLAWMVATELVAG----- 371
Db	190	EGSHENFYSNL	FSPGERKGV	WTSLCW-----	GIV--LSVLLYLS
Qy	372	-----	LLLGFEVFTLSHNG	KEYNESKDFVRAQV-----	ITRNTKRGWFNDWF 414
Db	238	LYGVFVLIFVMWLD	FVTYLLHHG---Y	THKLPWYRGQ	EWSYLRGG
Qy	415	TGGLDTQIEHHLE	FPTMPRENYEKI	APQVEALCKKH 449	
Db	294	HEDIGTHVIHH	LPQIPHYH	LV	NEATKSAKSVLGKY 328

Search completed: June 16, 2004, 19:06:19
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:06:22 ; Search time 46 Seconds
(without alignments)
3312.941 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTDFLNPLGLTWSKYSV.....AVVKALKEIADKASIRLHAH 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREXBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2595	100.0	483	10 Q9LEN0	Q9len0 ceratodon p
2	1619	62.4	520	10 Q9LEM9	Q9lem9 ceratodon p
3	1475	56.8	525	10 Q9ZNM2	Q9znm2 physcomitre
4	841.5	32.4	457	3 Q9UVV3	Q9uvv3 mortierella
5	840.5	32.4	457	3 Q8X173	Q8x173 mortierella
6	839.5	32.4	457	3 Q9UVY3	Q9uvy3 mortierella
7	835.5	32.2	457	3 Q9HEY4	Q9hey4 mortierella
8	821.5	31.7	457	3 Q8X174	Q8x174 mortierella
9	821.5	31.7	457	3 Q9HEY1	Q9hey1 mortierella
10	799.5	30.8	477	10 Q8RXB0	Q8rxbo phaeodactyl
11	793	30.4	459	10 Q944W4	Q944w4 pythium irr
12	743.5	28.7	458	3 Q7Z8P2	Q7z8p2 rhizopus sp
13	705.5	27.2	467	3 Q96VC3	Q96vc3 mucor circi
14	668.5	25.8	357	3 Q9HDF4	Q9hdf4 mortierella
15	603.5	23.3	458	10 Q43469	Q43469 helianthus
16	587	22.6	449	10 Q9ZRP7	Q9zrp7 arabidopsis

17	584	22.5	449	10 Q8LB96	Q8lb96 arabidopsis
18	583	22.5	449	10 Q9ZRP8	Q9zrp8 brassica na
19	582.5	22.4	446	10 Q8LLD7	Q8lld7 aquilegia v
20	574	22.1	419	10 Q9SWQ9	Q9swg9 euglena gra
21	574	22.1	448	10 Q04353	Q04353 borago offi
22	574	22.1	453	10 Q84KG8	Q84kg8 primula far
23	573	22.1	448	10 Q9SAU5	Q9sau5 borago offi
24	569.5	21.9	446	10 Q9ZTY9	Q9zty9 ricinus com
25	568	21.9	448	10 Q8VZZ2	Q8vzz2 echium gent
26	563	21.7	453	10 Q84KG6	Q84kg6 primula via
27	560	21.6	452	10 Q84KG7	Q84kg7 primula via
28	559	21.5	443	5 Q61388	Q61388 caenorhabdi
29	558	21.5	443	5 Q23221	Q23221 caenorhabdi
30	558	21.5	448	10 Q8VZZ1	Q8vzz1 echium pita
31	557	21.5	452	10 Q84KG9	Q84kg9 primula far
32	554.5	21.4	501	4 Q8NCC7	Q8ncc7 homo sapien
33	554.5	21.4	501	4 Q8NCG0	Q8ncg0 homo sapien
34	551	21.2	446	10 Q9FR82	Q9fr82 borago offi
35	550	21.2	444	4 Q96I39	Q96i39 homo sapien
36	550	21.2	444	4 Q96T10	Q96t10 homo sapien
37	549	21.2	444	4 Q60427	Q60427 homo sapien
38	546	21.0	444	4 Q9NRP8	Q9nrp8 homo sapien
39	546	21.0	444	4 Q9NYX1	Q9nyx1 homo sapien
40	535	20.6	444	4 Q96SV3	Q96sv3 homo sapien
41	528.5	20.4	447	11 Q920R3	Q920r3 rattus norv
42	528	20.3	444	4 Q95864	Q95864 homo sapien
43	528	20.3	448	10 Q8L7I7	Q8l7i7 argania spi
44	527.5	20.3	447	11 Q920L1	Q920l1 mus musculu
45	526.5	20.3	447	11 Q8VC07	Q8vc07 mus musculu

ALIGNMENTS

RESULT 1
Q9LENC
ID Q9LENO PRELIMINARY; PRT; 483 AA.
AC Q9LENO;
DT Q1-OCT-2000 (TrEMBLrel. 15, Created)
DT Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Delta 6-fatty acetylase.
OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
OX NCBI_TaxID=3225;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt3; TISSUE=Protonemata;
RX MEDLINE=20307617; PubMed=10848999;
RA Sperling P., Lee M., Girke T., Zaehrer U., Stymne S., Heinz B.;
RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the moss Ceratodon purpureus. A new member of the cytochrome b5 superfamily.";
RT Eur. J. Biochem. 267:3801-3811 (2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ250734; CAB94992.1; --
DR HSSP; P04166; 1B5M.
DR GC; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 483 AA; 54857 MW; C451D0042169AB1C2 CRC64;

Query Match 100.0%; Score 2595; DB 10; Length 483;
Best Local Similarity 100.0%; Pred.No. 5.4e-217;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVTDFLNFLGTTWSKYSVYTHSYAGNYGPTLKHAKVSAQKTAGQTLRQRSVQDKKP 60
Db |||||
QY 61 GTYSLADVASHDRPGDCMWIVKEKVYDISRFADDPHGPGTVISTYFGRDGTDFATFHPPA 120
Db |||||
QY 121 AWKQLNDYVIGDLAREEPLDELLKVDYDRAEFVREGLFKSSKAWFLLOTLINAALFAAS 180
Db |||||
QY 181 IATICYDKSYWAIIVLSASLMGLFVQQCGWLAHDFLHQOVFENRTANSFFGYLFGNCVLGF 240
Db |||||
QY 241 SVSWWRTKHNIIHTAPNECDEQYTPLEDEDITLPIIAWSKEILATVESKRILRVLYQYQHY 300
Db |||||
QY 301 MILPLLFMARYSWTFGSLFTFNPDLSTTKGLIEKGTVAFYAWFSAARFHLPGVAKPL 360
Db |||||
QY 361 ANMVATELVAGLLGLGFVFTLSHNGKEVYNESKDFVRAQVITTRNTKRGWENDWFTGGLDT 420
Db |||||
QY 421 QIEHHLFPTMPRHNYPKIAPOVEALCKKHGLEVDNVSVVGASVAVVKALKEIADEASIRL 480
Db |||||
QY 481 HAH 483
Db |||||
QY 481 HAH 483

RESULT 2
Q9LEM9 PRELIMINARY; PRT; 520 AA.
ID Q9LEM9
AC Q9LEM9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Delta 6-fatty acid desaturase.
OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
OX NCBI_TaxID=3225;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wt3; TISSUE=Protonemata;
RX MEDLINE=20307617; PubMed=10848999;
RA Sperling P., Lee M., Girke T., Zaehring U., Stymne S., Heinz E.;
RT "A bifunctional delta 6-fatty acyl acetylenase/desaturase from the
RT moss Ceratodon purpureus. A new member of the cytochrome b5
RT superfamily";
RL Eur. J. Biochem. 267:3801-3811(2000).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ250735; CAB94993.1; -.
DR HSSP; P00171; IEHB.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 520 AA; 59160 MW; 5A9332EECC153439 CRC64;

Query Match 62.4%; Score 1619; DB 10; Length 520;

Best Local Similarity 61.5%; Pred. No. 4.8e-132;
Matches 302; Conservative 72; Mismatches 101; Indels 16; Gaps 3;
QY 1 MALVTDFLNFLGTTWSKYSVYTHSYAGNYGPTLKHAKVSAQ-----GKTA 46
Db |||||
QY 47 GQTLRQSVQDKKPGTYSLADVASHDRPGDCMWIVKEKVYDISRFADDPHGPGTVISTYFG 106
Db |||||
QY 84 AQPIRRRWVQDKKPGTYSLKDVASHDMPQDCWIIKEKVYDSTFAEQHEGTVINTYFG 143
QY 107 RDGTDVFATFHPPAAWKQLNDYVIGDLAREEPLDELLKDYRDMRAEFVREGLFKSSKAWF 166
Db |||||
QY 144 RDATDVFSTPHASTSWKILQNFYIGNLVREPTLELLKEYRELRLALFLREQLFKSSKSY 203
QY 167 LLOTLINAALFAASIATICYDKSYWAIIVLSASLMGLFVQQCGWLAHDFLHQOVFENRTAN 226
Db |||||
QY 204 LFKTLINVSIVATSIATISLYKSYRAVLLSASLMGLFIQQCGWLSHDFLHHQVETRWN 263
QY 227 SFFGYLSCNVLGFSVSWWRTKHNIIHTAPNECDEQYTPLEDEDITLPIIAWSKEILATV 286
Db |||||
QY 264 DVVGYYWGVVVLGFSVSWWTKHNLEHAAPNECDQKYPIDEDIDTLPIIAWSKDLLATV 323
QY 287 ESKRILRVLYQYQHYMILPLLFMARYSWTFGSLFTFNPDLSTTKGLIEKGTVAFYAWFS 346
Db |||||
QY 324 ESKTMLRVLYQYQHLFFLVLLTFARASLFWSAFTLRPELTGKLLERGTMAHLYWFN 383
QY 347 WAAFHILPGVAKPLAMVATELVAGLLGLGFVFTLSHNGKEVYNESKDFVRAQVITTRNTK 406
Db |||||
QY 384 SVAFYLLPG-WKPVVWVWVSELMSGFLLGVFVLSHNGMEVYNTSKDFVNAQIASTRDIK 442
QY 407 RGFENDWFTGGLDTQIEHHLFPTMPRHNYPKIAPOVEALCKKHGLEVDNVSVVGASVAVV 466
Db |||||
QY 443 AGVFENDWFTGGLNRQIEHHLFPTMPRHNLNKISPHVETLCKKHGLVYEDVSMASGTYRVL 502
QY 467 KALKEIADEAS 477
Db |||||
QY 503 KTLKDVADAAS 513

RESULT 3
Q9ZNW2 PRELIMINARY; PRT; 525 AA.
ID Q9ZNW2
AC Q9ZNW2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DELTA6-acyl-lipid desaturase.
GN DES6.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEDW. B. S. G;
RX MEDLINE=98416756; PubMed=9744093;
RA Girke T., Schmidt H., Zaehring U., Reski R., Heinz E.;
RT "Identification of a novel delta 6-acyl-group desaturase by targeted
RT gene disruption in Physcomitrella patens";
RL Plant J. 15:39-48(1998).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ222981; CAA11033.1; -.
DR EMBL; AJ222980; CAA11032.1; -.
DR HSSP; P04166; IICC.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.

DR	ProDom; PD001081; FA desat_fam; 2.	DR	ProDom; PD001081; FA desat_fam; 2.
DR	PROSITE; PS00191; CYTOCHROME_B5_1; 1.	DR	PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.	DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW	Heme.	KW	Heme.
SQ	SEQUENCE 457 AA; 51784 MW; 7E8CE779CE9E928A CRC64;	SQ	SEQUENCE 457 AA; 51816 MW; 5C4B3D7312439543 CRC64;
Query Match			
Best Local Similarity 32.4%; Score 840.5; DB 3; Length 457;			
Matches 172; Conservative 70; Mismatches 149; Indels 35; Gaps 9;			
QY	79 YIVKEKVDISRFADCHPGGTIVSTYFGRDGTDFVATEFHPPAWKQLNDYYIGDLAREEP 138	QY	79 MIVKEKVDISRFADCHPGGTIVSTYFGRDGTDFVATEFHPPAWKQLNDYYIGDLAREEP 138
Db	34 MIIDNKVYDVREFVDPHGGSVILTHVKGKGTDFVDFTFHPEAAWETLANFYVGDIDESDR 93	Db	34 MIIDNKVYDVREFVDPHGGSVILTHVKGKGTDFVDFTFHPEAAWETLANFYVGDIDESDR 93
QY	139 L---DELLKDYRDMRAEFVREGLFKSSKAWFLLQTLINAALEFAASIATICY--DKSYWAI 193	QY	139 L---DELLKDYRDMRAEFVREGLFKSSKAWFLLQTLINAALEFAASIATICY--DKSYWAI 193
Db	94 AIKNDDFAAEVRKLTFLFQSLGYDSSKAYYAFKVSFNLCIWGLSTFIIVAKWGQTSTLAN 153	Db	94 AIKNDDFAAEVRKLTFLFQSLGYDSSKAYYAFKVSFNLCIWGLSTFIIVAKWGQTSTLAN 153
QY	194 VLSASLMGLFVQCCGWLADHFLHQOVFNENRTANSEFGYLFNCVLFSGSVSWMRTKHNHH 253	QY	194 VLSASLMGLFVQCCGWLADHFLHQOVFNENRTANSEFGYLFNCVLFSGSVSWMRTKHNHH 253
Db	154 VLSAALLGLFWQCCGWLADHFLHQOVFQDRFWGDLFGAFLGGVCCGFSSSWWKDKHNTHH 213	Db	154 VLSAALLGLFWQCCGWLADHFLHQOVFQDRFWGDLFGAFLGGVCCGFSSSWWKDKHNTHH 213
QY	254 TAPNECEQYTPLEDEDIDTLPILAWSK---EILATVESKRILRVLYQHYMIL----- 303	QY	254 TAPNECEQYTPLEDEDIDTLPILAWSK---EILATVESKRILRVLYQHYMIL----- 303
Db	214 AAPNVHGE-----DPDIDTHPLLTWSEHALEMFSVPDEELTRM--WSRFMVLNQTWEIF 266	Db	214 AAPNVHGE-----DPDIDTHPLLTWSEHALEMFSVPDEELTRM--WSRFMVLNQTWEIF 266
QY	304 PLLFMARYSWTFGSLFTFNPDLSITK-----GLIEKGTVAHFYAWFSAAFHILPG 355	QY	304 PLLFMARYSWTFGSLFTFNPDLSITK-----GLIEKGTVAHFYAWFSAAFHILPG 355
Db	267 PILSFARLSWCLQSILFVL-PNGQAHKPSGARVPISLVEQLSLAVHWTYLATMELFIKD 325	Db	267 PILSFARLSWCLQSILFVL-PNGQAHKPSGARVPISLVEQLSLAMHTWTYLATMELFIKD 325
QY	356 VAKPLAMWVATELVAGLLGFVFTLSHNGKEVYNESK----DFVRAQVITTRNTKRGWEN 411	QY	356 VAKPLAMWVATELVAGLLGFVFTLSHNGKEVYNESK----DFVRAQVITTRNTKRGWEN 411
Db	326 PVMNVYFLVSQAVCGNLLAIVFSLNHNMGMPVISKEEAADMDFETKQIITGRDVHPGLFA 385	Db	326 PVMNVYFLVSQAVCGNLLAIVFSLNHNMGMPVISKEEAADMDFETKQIITGRDVHPGLFA 385
QY	412 DWFTGGLDTQIEHHLFPTMPRHNPYKPIAPQVEALCKKHGLEVDNVSVVGASVAVVKALKE 471	QY	412 DWFTGGLDTQIEHHLFPTMPRHNPYKPIAPQVEALCKKHGLEVDNVSVVGASVAVVKALKE 471
Db	386 NWFTGGLNYQIEHHLFPTMPRHNFESKIOPAVETLCKKYGVRYHTTGMIEGTAEVFSRLNE 445	Db	386 NWFTGGLNYQIEHHLFPTMPRHNFESKIOPAVETLCKKYGVRYHTTGMIEGTAEVFSRLNE 445
QY	472 IADEAS 477	QY	472 IADEAS 477
Db	446 VSKAAS 451	Db	446 VSKAAS 451
RESULT 6			
Q9UVY3	PRELIMINARY; PRT; 457 AA.	Q9HEY4	PRELIMINARY; PRT; 457 AA.
AC	Q9UVY3	AC	Q9HEY4
DT	01-MAY-2000 (TremBLrel. 13, Created)	DT	01-MAR-2001 (TremBLrel. 16, Created)
DT	01-MAY-2000 (TremBLrel. 13, Last sequence update)	DT	01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT	01-JUN-2003 (TremBLrel. 24, Last annotation update)	DT	01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE	Delta-6 fatty acid desaturase.	DE	Delta6-fatty acid desaturase.
OS	Mortierella alpina.	OS	Mortierella isabellina (Umbelopsis isabellina).
OC	Eukaryota; Fungi; Zygomycota; Mortierellales;	OC	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC	Mortierellaceae; Mortierella.	OC	Mucorales incertae sedis; Umbelopsis.
OX	NCBI_TaxID=64518;	OX	NCBI_TaxID=91625;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN-1S-4;	RA	Ming-Chun L., Li L., Guo-Wu H., Li Z., Lai-Jun X.;
RX	MEDLINE=20035749; PubMed=10570972;	RT	"Cloning and sequencing analysis of delta6-fatty acid desaturase gene from Mortierella isabellina.";
RA	Sakuradani E., Kobayashi M., Shimizu S.;	RL	Junwu Xitong 0:0-0(2001).
RT	"Delta 6-Fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a fungus, Aspergillus.";	CC	-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
RL	Gene 238:445-453(1999).	DR	EMBL; AF306634; AAG38104.1; --
CC	-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.	DR	HSSP; P04166; 1EUE.
DR	EMBL; AB020032; BAA85588.1; --	DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
DR	HSSP; P04166; 1EUE.	DR	InterPro; IPR001199; Cyt_B5.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.	DR	InterPro; IPR005804; FA_desat_fam.
DR	InterPro; IPR001199; Cyt_B5.	DR	Pfam; PF00487; FA_desaturase; 1.
DR	Pfam; PF00487; FA_desaturase; 1.	DR	Pfam; PF00173; heme_1; 1.
DR	Pfam; PF00173; heme_1; 1.	DR	ProDom; PD000612; Cyt_B5; 1.
DR	ProDom; PD000612; Cyt_B5; 1.	DR	PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR		DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.

KW Heme.
SQ SEQUENCE 457 AA; 51772 MW; 868E7EB21172D5AF CRC64;
Query Match 32.2%; Score 835.5; DB 3; Length 457;
Best Local Similarity 40.1%; Pred. No. 5.8e-64;
Matches 171; Conservative 70; Mismatches 150; Indels 35; Gaps 9;
Qy 79 MIVKEKYDISRFAEDHPPGGTVISTYFGRDGTDFATFHPAANKQLNDYIGDLAREEP 138
Db 34 MIIDNKYDVREVPDPHGGSVILTHVGKDGTDVDTFHPPEAAWETLANFYVGDIDESDR 93
Qy 139 L---DELLKDYRDMRAEFVREGLFKSSKAWFELLQTLINAALFAASIATICY--DKSYWAI 193
Db 94 AIKNDFFAAEVRKLRITLFSQSLGYDSSKAYYAFKVSFNLCIWGLSTFIVAKWGQTSTLAN 153
Qy 194 VLSASLMGLFVQCCGWLADFLHQVFNRTANSEFFGYLFGNCVLFGSVSWRTKHNH 253
Db 154 VLSAALLGLFWQCCGWLADFLHQVFNRTANSEFFGYLFGNCVLFGSVSWRTKHNTHH 213
Qy 254 TAPNECEQYTPLEDDEDITLPIIAWSK---EILATVESKRILRVLYQYQHYMIL----- 303
Db 214 AAPNVHGE-----DPDIDTHPLLTWSEHALEMFSDDVPDEELTRM--WSRFVNLQTWFFYF 266
Qy 304 PLLFMARYSWTFGSLLETFNPDLSSTTK-----GLIEKGTVAHYAFWSAAAFHILPG 355
Db 267 PILSPARLSWCLQSILLVL-PNGQAHKESGARVSISLVEQLSLAMHWTWYLATMFLFIKD 325
Qy 356 VAKPLAWVATELVAGLLGFVFTLSHNGKEVYNESK---DFVRAQVITTRNTKRGWFN 411
Db 326 PVNMMVFLVSQAVCGNLLAIVFSLNHNMPVISKEEAVDMDFTKQIITGRDVHPGLFA 385
Qy 412 DWFTGGLDTQIEHHLFPTMPRHNYPKIAPQVEALCKKHGLEYNVSVVGASVAVVKALKE 471
Db 386 NWFTGGLNYQIEHHLFSPMRHNFSKIQPAVETLCKKYGVRYHTTGMIEGTAEVFSRLNE 445
Qy 472 IADEAS 477
Db 446 VSKAAS 451

RESULT 8
Q8X174 PRELIMINARY; PRT; 457 AA.
ID Q8X174
AC Q8X174;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Delta 6 fatty acid desaturase.
GN GLD6D.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 16266;
RA Liu L., Li M., Hu G., Xing L.;
RT "Cloning and sequence analysis of the delta 6 fatty acid desaturase gene from Mortierella alpina ATCC16266 genomic and cDNA.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF465281; AAL73947.1; --.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA; 51915 MW; 087B91DC47F2EDA3 CRC64;

Query Match 31.7%; Score 821.5; DB 3; Length 457;
Best Local Similarity 39.9%; Pred. No. 9.6e-63;
Matches 170; Conservative 70; Mismatches 151; Indels 35; Gaps 9;
Qy 79 MIVKEKYDISRFAEDHPPGGTVISTYFGRDGTDFATFHPAANKQLNDYIGDLAREEP 138
Db 34 MIIDNKYDVREVPDPHGGSVILTHVGKDGTDVDTFHPPEAAWETLANFYVGDIDESDR 93
Qy 139 L---DELLKDYRDMRAEFVREGLFKSSKAWFELLQTLINAALFAASIATICY--DKSYWAI 193
Db 94 AIKNDFFAAEVRKLRITLFSQSLGYDSSKAYYAFKVSFNLCIWGLSTFIVAKWGQTSTLAN 153
Qy 194 VLSASLMGLFVQCCGWLADFLHQVFNRTANSEFFGYLFGNCVLFGSVSWRTKHNH 253
Db 154 ELSAALLGLFWQCCGWLADFLHQVFNRTANSEFFGYLFGNCVLFGSVSWRTKHNTHH 213
Qy 254 TAPNECEQYTPLEDDEDITLPIIAWSK---EILATVESKRILRVLYQYQHYMIL----- 303
Db 214 AAPNVHGE-----DPDIDTHPLLTWSEHALEMFSDDVPDEELTRM--WSRFVNLQTWFFYF 266
Qy 304 PLLFMARYSWTFGSLLETFNPDLSSTTK-----GLIEKGTVAHYAFWSAAAFHILPG 355
Db 267 PILSPARLSWCLQSILLVL-PNGQAHKESGARVSISLVEQLSLAMHWTWYLATMFLFIKD 325
Qy 356 VAKPLAWVATELVAGLLGFVFTLSHNGKEVYNESK---DFVRAQVITTRNTKRGWFN 411
Db 326 PVNMMVFLVSQAVCGNLLAIVFSLNHNMPVISKEEAVDMDFTKQIITGRDVHPGLFA 385
Qy 412 DWFTGGLDTQIEHHLFPTMPRHNYPKIAPQVEALCKKHGLEYNVSVVGASVAVVKALKE 471
Db 386 NWFTGGLNYQIEHHLFSPMRHNFSKIQPAVETLCKKYGVRYHTTGMIEGTAEVFSRLNE 445
Qy 472 IADEAS 477
Db 446 VSKAAS 451

RESULT 9
Q9HEY1 PRELIMINARY; PRT; 457 AA.
ID Q9HEY1
AC Q9HEY1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Delta 6-fatty acid desaturase.
GN GLD6D-I.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RA Xing L., Li M., Liu L., Hu G., Zhang L.;
RT "Expression of Mortierella alpina delta 6-fatty acid desaturase gene in Saccharomyce cerevisiae.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 16266;
RA Liu L., Li M., Hu G., Xing L.;
RT "Cloning and sequence analysis of the delta 6 fatty acid desaturase gene from Mortierella alpina ATCC16266 genomic and cDNA.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF307940; AAG45092.1; --.
DR EMBL; AF465283; AAL73949.1; --.
DR HSSP; P04166; IEUE.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.

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QY 162 SKAWFL--LQTLNAAALFAASIAITCYDKSYWAIVLASLMLGLFVQCCGLAHDFLHQV 219
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 STGFYIKVSTLLVCIVGLAILKAWGRESTLAVFIAASLVGLFWQCCGLAHDAHYQV 189
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 220 FENRTANSFFGYLFGNCVLFVSWSWRTKXNIHHTAPNECDEQYTPLEDEIDTLPPIAWS 279
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 IKDPNVNLFVLVTGFLVQGFSLSWKXKXNTHASTNVSGE-----DPDIDTAPILLWD 244
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 280 KEIATVESK-----RIL--RVLYQYHMYLPLLFMARYSWTEGSLLETF--NPDL 327
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 BEAVANFYGLKDNASGDFRFAIEHILPYQTRYYPFILGFARTSWAIQSIISYFKNETLN 304
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 328 TTKGL--LEKGTVAFYAWESWAAAFHILPGVAKPLAWMVATLVAGLLGLGFVFTLSHNGK 385
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 KSKLSWCERIFLVHVVFFTYCTIAWISSIRNIAMFFVVSQITTYGILLAIIVFAMNHNGM 364
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 386 EYNESK---DEVRAQVITTRNTKRGWENDWFTGGLDTQIEHELEPTMPRHNYPKIAPQ 441
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 PVYSPEANHTFEFYLQICITGRDVNCTVFGDWLMGGLNYQIEHELEFPEMPRHLSKVKSM 424
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 442 VEALCKKHGLEVDNVSVWGASVAVVKAL 469
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 VKPIAQKYNIPYHDTTVIGGTIEVLQTL 452
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 14

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Q9HDF4 ID Q9HDF4 PRELIMINARY; PRT; 357 AA.
AC Q9HDF4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Delta 6-fatty acid desaturase (Fragment).
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RA Xing L., Li M., Liu L., Hu G., Zhang L.;
RT "Cloning and sequence analysis of the conserved region of delta 6-
RT fatty acid desaturase gene from Mortierella alpina.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Xing L., Li M., Liu L., Hu G., Zhang L.;
RT "Cloning and sequence analysis of the conserved region of delta 6-
RT fatty acid desaturase gene from Mortierella alpina.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307942; AAG45094.1; -
DR EMBL; AF307941; AAG45093.1; -
DR HSSP; P04166; 1EJE.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001139; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
FT NON_TER 1
FT NON_TER 357
SQ SEQUENCE 357 AA; 40796 MW; C8D9CE1283BB16B8 CRC64;
```

Query Match 25.8%; Score 668.5; DB 3; Length 357;

Best Local Similarity 39.2%; Pred. NO. 1.4e-49;

Matches 143; Conservative 59; Mismatches 128; Indels 35; Gaps 9;

```
QY 91 FADDPGGTVISTYFGRDGTDFATEHPPAWKLNDYIIGDLAREPL---DELLKOYR 147
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 FVPDHPGGSVILTHVKGDTDFDTFHPAAWETLANFYVGIDESRAIKNDFFAAEVR 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 148 DMRAEFVRBGLFKSKAWFLLOTLNAAALFAASIAITCY--DKSYWAIVLASLMLGLFVQ 205
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 KLRTLFQSLGYDSSKAYYAEKVSFNLCLWGLSTFIVAKRGQTSTLANELSAALLGLFWQ 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 206 QCGWLAHDFLHQVFEENRTANSFFGYLFGNCVLFVSWSWRTKXNIHHTAPNECDEQYTP 265
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 QRGWLAHDFLHQVFEQDRFWGLDFGALFGDCQGFSSSWKXKXNTHHAAPNVHGE---- 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 266 LDEDIDTLPPIAWSK---EILATVESKRLRVLYQYHMYL-----PLLFMARYSWTF 315
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 -DPDIDTLPPIAWSK---EILATVESKRLRVLYQYHMYL-----PLLFMARYSWTF 233
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 316 GSLLFTFNPDLSSTK-----GLIEKGTVAFYAWESWAAAFHILPGVAKPLAWMVATE 367
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 QSILFVL-PNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDPVNMVYFLVSQ 292
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 368 LVAGLLGLGFVFTLSHNGKEVYNESK---DFVRAQVITTRNTKRGWENDWFTGGLDTQIE 423
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 293 AVCGNLLAIVFSLNHNMGMPVISKEEAVDMDFFTKQIITGRDVHFGFLFANWFTGGLNYQIE 352
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 424 HHLFP 428
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 353 HHLFP 357
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 15

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Q43469 ID Q43469 PRELIMINARY; PRT; 458 AA.
AC Q43469;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Delta-8 sphingolipid desaturase.
GN SLD1.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Asteroidae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. inbred line HA89;
RC TISSUE=Cotyledons of developing sunflower fruits;
RX MEDLINE=96028121; PubMed=7586718;
RA Sperling P., Schmidt H., Heinz E.;
RT "A cytochrome b5-containing fusion protein similar to plant acyl lipid
RT desaturases.";
RL Eur. J. Biochem. 232:798-805(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. inbred line HA89;
RC TISSUE=Cotyledons of developing sunflower fruits;
RX MEDLINE=21116801; PubMed=11171153;
RA Sperling P., Blume A., Zaehrer U., Heinz E.;
RT "Further characterization of delta 8-sphingolipid desaturases from
RT higher plants.";
RL Biochem. Soc. Trans. 28:638-641(2000).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; X87143; CAA60621.1; -.
DR EMBL; X87143; CAA60621.1; -.
DR HSSP; P00171; 1F03.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 458 AA; 52231 MW; D182287AB0E99245 CRC64;
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Query Match		23.3%;	Score 603.5;	DB 10;	Length 458;
Best Local Similarity		31.1%;	Pred. No. 8.9e-44;		
Matches 136;		Conservative 85;	Mismatches 193;	Indels 23;	Gaps 8;
QY	54	SVQDKKPGTYSLADWASHDRPGDCNMIVKEKVVYDISRFADDPGGIV-ISTYFGRDGTDV	112		
Db	11	SIADGKKYITS-KELKKHNNPNDLWISILGKVNVTWAKEHPGGDAPLINLAGQDVTDA	69		
QY	113	FATFHPPAWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFVREGLFKSSKAWFLLOTLI	172		
Db	70	FIAFHPGTANKHLDKLFYTGHLKDYQVSDISRDYRKLASEFAKAGMFEKKHGVISLCF	129		
QY	173	NAALFAASIATICYDKSYWAIJVLASLMGLFVQQCGWLAHDFLHQVFNERTANSFFGYL	232		
Db	130	VSLLLSACVVGVIYSGSFWIHMLSGAILGLAWMCIAYLGHDAAGHYQMATRGWNKFAGIF	189		
QY	233	FGNCVLGFSVSWRTKHNHTAPNECDEQVTPLDDEDIDTLPZIAWSKEILATVESKRIL	292		
Db	190	IGNCITGISIAWKKWTHNAHIAACNSLD-----YCPDLQHLPLMAVSSKLFNSITSVEYG	244		
QY	293	RVL-----QYQHMYMILPILLEMARYSWTEGSLLETFNPDLSSTTKGLIEKGTVAHY	342		
Db	245	RQLTDFPLARFFVSQYHYLYYPIMCVARVNLVLTIELLISKRKIPDRGLNILGTLIF-W	303		
QY	343	AWFSWAAEHILPGVAKPLAWMVATELVAGLLLGFWFTLSHNGKEYV---NESKDFVRAQV	399		
Db	304	TWFPLLVSR-LPNWPERVAFLVSVFCVTG-IQHIQFTLNHFSGDVYVGPVKGDNWFEEKQT	361		
QY	400	ITTRNTKRGWENDWFTGGLDTOIEHHLFPTWPRHNYPKIAPQVEALCKKHGLEVDNVSVV	459		
Db	362	RGTDIDACSSWMDWFFGGGLQFQLEHHLFPRLPRCHLRSISPICRELCKKNLPPVVSLSFY	421		
QY	460	GASVAVVVKALKELADEA	476		
Db	422	DANVTTLKTLRTAALQA	438		

Search completed: June 16, 2004, 19:10:42
Job time : 49 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2004, 02:36:30 ; Search time 3746 Seconds
(without alignments)
3850.356 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTDFLNLGLTTSKYSV.....AVVKALKEIADEASIRLHAH 483

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DOCALIGN=200 -THR SCORE=pt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pt -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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21: em_gss_fun:*
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26: em_gss_phg:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	652	25.1	753	12	BJ579910	BJ579910 BJ579910
C 2	649	25.0	764	12	BJ169984	BJ169984 BJ169984
C 3	634	24.4	688	12	BJ170744	BJ170744 BJ170744
C 4	617	23.8	728	12	BJ597842	BJ597842 BJ597842
C 5	583	22.5	697	12	BJ599570	BJ599570 BJ599570
C 6	583	22.5	698	12	BJ604593	BJ604593 BJ604593
7	567.5	21.9	1764	11	AY103762	AY103762 Zea mays
8	539	20.8	519	12	BQ040185	BQ040185 gd12e11.y
9	529	20.4	2272	11	AK076485	AK076485 Mus muscu
10	528	20.3	1335	29	AY418548	AY418548 Homo sapi
11	527.5	20.3	3318	11	AK083959	AK083959 Mus muscu
C 12	517	19.9	622	10	AW476747	AW476747 ga37d12.y
13	516	19.9	1689	11	AK080414	AK080414 Mus muscu
14	514	19.8	3129	11	AK029318	AK029318 Mus muscu
15	503	19.4	1335	29	AY418550	AY418550 Mus muscu
C 16	499	19.2	746	12	BJ583356	BJ583356 BJ583356
C 17	479	18.5	766	12	BJ600861	BJ600861 BJ600861
18	478	18.4	3697	11	AK090042	AK090042 Mus muscu
C 19	443.5	17.1	699	12	BJ597953	BJ597953 BJ597953
C 20	443.5	17.1	700	12	BJ599342	BJ599342 BJ599342
C 21	443.5	17.1	726	12	BJ603698	BJ603698 BJ603698
22	441.5	17.0	1131	29	AY420234	AY420234 Homo sapi
23	439	16.9	2862	11	AK083282	AK083282 Mus muscu
C 24	438	16.9	480	12	BJ599078	BJ599078 BJ599078
25	428.5	16.5	1131	29	AY420236	AY420236 Mus muscu
C 26	409	15.8	522	12	BJ601553	BJ601553 BJ601553
27	409	15.8	985	14	CB264523	CB264523 55-E02082
28	401.5	15.5	1079	29	AY420235	AY420235 Pan trogl
C 29	392.5	15.1	507	12	BJ173747	BJ173747 BJ173747
30	382	14.7	867	29	CG847823	CG847823 ZMMBB031
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32	376	14.5	696	13	BQ861565	BQ861565 QGC18P18.
33	375	14.5	786	14	CD837141	CD837141 BN45.051D
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35	370.5	14.3	934	29	CG264599	CG264599 CGWGP72TV
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37	367.5	14.2	817	14	CB893839	CB893839 EST646531
38	366	14.1	756	13	BU025934	BU025934 QHGI2E03.
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40	364.5	14.0	914	29	CG463170	CG463170 PUTJP24TD
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42	361	13.9	655	13	BU026750	BU026750 QHGI7O20.
43	359	13.8	745	13	BU026884	BU026884 QHGI8G02.
44	359	13.8	765	13	BU024179	BU024179 QHFI6J23.
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ALIGNMENTS

RESULT 1
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LOCUS BJ579910 753 bp mRNA linear EST 22-OCT-2003
DEFINITION BJ579910 normalized full length cDNA library, chloronemata, caulonemata and malformed buds Physcomitrella patens subsp. patens cDNA clone pphb12117 3', mRNA sequence.
ACCESSION BJ579910
VERSION BJ579910.1 GI:37821844
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE	1 (bases 1 to 753)		
AUTHORS	Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H., Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,M.		
TITLE	Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)		
MEDLINE	22709184		
PUBMED	12808149		
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector(5'- gagAgAgAggATCCAAACCTGGAgAgTTTTTTTTTTTTTTVN-3' was used as a 1st 3' primer, and 5'-ggTTCGAgTCATCGTGTTCAGACgAgTCgATGCTGAgAACCGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGCGGAGCTCGAATTCGCGAACCG). cDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003). Protonemata were blended by the POLYTRON, and then cultivated on the BCDAG medium for 13- 14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHYSCobase (http://moss.nibb.ac.jp).		
FEATURES	Location/Qualifiers 1..753 /organism="Physcomitrella patens subsp. patens" /mol_type="mRNA" /sub_species="patens" /db_xref="taxon:14548" /clone="pphb12117" /tissue_type="mixture of chloronemata, caulonemata and malformed buds" /clone_lib="normalized full length cDNA library, chloronemata, caulonemata and malformed buds"		
ORIGIN			
Alignment Scores:			
Pred. No.:	2.43e-68	Length:	753
Score:	652.00	Matches:	126
Percent Similarity:	73.56%	Conservative:	25
Best Local Similarity:	61.46%	Mismatches:	52
Query Match:	25.13%	Indels:	2
DB:	12	Gaps:	2
US-09-980-468-2 (1-493) x BJ579910 (1-753)			
QY	278	TrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgValLeuGlnTyr	297
Db	752	TGGAGCAAGGACATACTGGCCACAGTTGAGAATAAGACATCTTTCGAATCTCCAATAC	693
QY	298	GlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThrPheGlySer	317
Db	692	CAGCATCTGTTCTTCATGGGTCTGTATTTCGCCCGTGGTGTGCTCTTTTGGAGC	633
QY	318	LeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGlyThr	337
Db	632	TGGAGATATACCTCTACAGCAGTGTCTCTACCTGTGTCGACAGGTTGTGGAGAGGAACT	573
QY	338	ValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuProGlyValAla	357
Db	572	GTTCTGTTTCACTACTTTTGGTTCGTGGGACAGCGTGCTATCTTCTCCCTGGT---	TGG 516
QY	358	LysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeuGlyPheVal	377
Db	515	AAGCCATTAGTATGGATGCGGTGACTGAGTCATGTCGGCATGCTGCTGGCTTTGTA	456
QY	378	PheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheValArgAla	397
Db	455	TTTGTACTTAGCCACAATGGGATGGAGGTTTATAATTCGTCTAAGAAATTCGTGAGTGCA	396
QY	398	GlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThrGlyGly	417
Db	395	CAGATCGTATCCACACGCGGATATCAAGGAAACATATTCAACGACTGGTTCATGCTGGC	336
QY	418	LeuAspThrGlnIleGluHisLeuPhePheProThrMetProArgHisAsnTyrProLys	437
Db	335	CTTAACAGGCAAAATAGAGCATCTCTTTTCCCAACAATGCCAGGCATAATTAAACAAA	276
QY	438	IleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsnValSer	457
Db	275	ATAGCACCTAGAGTGGAGGTGTTCTCTGTAAAGAACACGGTCTGGTGTACGAGACGTATCT	216
QY	458	valValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAlaSer	477
Db	215	ATTGCTACCGGCACCTTGCAAGGTTTGAAGCATTTGAAGGAAGTCGCG---	GAGGCTGCG 159
QY	478	IleArgLeuHisAla	482
Db	158	GCAGAGCAGCATGCT	144
RESULT 2			
BJ169384/c			
LOCUS	BJ169984	764 bp	mRNA linear EST 16-OCT-2003
DEFINITION	BJ169984 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pph24e05 3', mRNA sequence.		
ACCESSION	BJ169984		
VERSION	BJ169984.1	GI:18337960	
KEYWORDS	EST.		
SOURCE	Physcomitrella patens subsp. patens		
ORGANISM	Physcomitrella patens subsp. patens		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella. 1 (bases 1 to 764)		
AUTHORS	Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H., Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,M.		
TITLE	Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)		
MEDLINE	22709184		
PUBMED	12808149		
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector(5'- gagAgAgAggATCCAAACCTGGAgAgTTTTTTTTTTTTTTVN-3' was used as a 1st 3' primer, and 5'-ggTTCGAgTCATCGTGTTCAGACgAgTCgATGCTGAgAACCGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGCGGAGCTCGAATTCGCGAACCG). cDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).		

Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13- 14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCOBASE (<http://moss.nibb.ac.jp/>).

FEATURES
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Location/Qualifiers
1..764

/organism="Physcomitrella patens subsp. patens"
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/db_xref="taxon:145481"
/clone="pph24e05"
/tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"
/clone_lib="full length cDNA library, chloronemata and young gametophores"

ORIGIN

Alignment Scores:
Pred. No.: 5.91e-68 Length: 764
Score: 649.00 Matches: 127
Percent Similarity: 73.56% Conservative: 26
Best Local Similarity: 61.06% Mismatches: 53
Query Match: 25.01% Indels: 2
DB: 12 Gaps: 2

US-09-980-468-2 (1-483) x BJ169984 (1-764)

QY 275 IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal 294
Db 762 CTCATTGCCTGNAGCAAGGACATACTGGCCACAGTTGAGAAATAGACATTCTTGGCAATC 703
QY 295 LeuGlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr 314
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QY 315 PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
Db 642 TTTTGGAGCTGGAGATATACCTTCACAGCAGTGCTCTCACCTGTCGACAGGTTGTGGAG 583
QY 335 LysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuPro 354
Db 582 AAGGGAAGTCTGTTCTTCTACTACTTTTGGTTCGTCGGGACAGCGTGCTATCTTCTCCCT 523
QY 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374
Db 522 GGT---TGAAGCCATTAGTATGGATGGCGGTGACTGAGCTCATGTCCGGCATGTCTGTG 466
QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
Db 465 GGCCTTTGTATTGTACTTAGCCACAATGGGATGGAGGTTTATAATTCGTCTAAAGATTC 406
QY 395 ValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
Db 405 GTGAGTGCACAGATCGTATCCACACGGGATATCAAGGAACATATTTCAACGACTGGTTC 346
QY 415 ThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHisAsn 434
Db 345 ACTGGTGGCCTTAACAGGCCAATAGAGCATCATCTTTTCCCAACAATGCCAGGCATAAT 286
QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAsp 454
Db 285 TTAAACAATAATAGCACCTAGATGTGAGGTGTTCTGTAGAAACACCGTCTGGTGTACGAA 226
QY 455 AsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp 474
Db 225 GACGTATCTATTGCTACCGGCACTTGCAGGTTTGTGAAGCATTTGAAGGAAGTCGCG--- 169
QY 475 GluAlaSerIleArgLeuHisAla 482
Db 168 GAGGCTGGGCAGAGCAGCATGCT 145

RESULT 3
BJ170744/c
LOCUS
DEFINITION

BJ170744 688 bp mRNA linear EST 16-OCT-2003
BJ170744 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pph26120 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BJ170744.1 GI:18338720
EST.

Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens

Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 688)
Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Mishide,H.,
Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K.,
Kohara,Y. and Hasebe,M.

REFERENCE
AUTHORS

TITLE

Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
JOURNAL
MEDLINE
PUBMED

Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
22709184

COMMENT

Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript II (KS),

that was in vivo excised from a l-FLC phage vector (Carninci et al.

2001). 5' end of the cDNA that was digested with XhoI was ligated

to SalI site of the vector and the 3' end including polyA tail was

ligated to BamHI site of the

vector(5'- GAGAGAGAGAGATCCAACCTGGAGAGTTTTTTTTTTTTTTVN-3' was

used as a 1st 3' primer, and

5'-ggTCTCGAGTCATCGCTGTCCAGACAGCGATGACTCGAGAACCGNNNN-3' as 2nd

5'-hairpin primer, giving the following 5' boarder sequence,

AGGCCAATCGCCGAGCTCGAATTCGCGAGAACCG). cDNA instert could be

amplified with conventional T7 and T3 primers. This full-length

cDNA library was generated according to the method described in

Nishiyama et al. (2003).

Protonemata were blended by the POLYTRON, and then cultivated on

the BCDATG medium for 13- 14 days under the continuous light.

These clones are available from RIKEN Bio Resource Center

(<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database

of Physcomitrella EST clones is available at the PHYSCOBASE

(<http://moss.nibb.ac.jp/>).

FEATURES
source
Location/Qualifiers
1..688

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/mol_type="mRNA"
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ORIGIN

Alignment Scores:
Pred. No.: 3.37e-66 Length: 688
Score: 634.00 Matches: 124
Percent Similarity: 73.04% Conservative: 25
Best Local Similarity: 60.78% Mismatches: 53
Query Match: 24.43% Indels: 2
DB: 12 Gaps: 2

US-09-980-468-2 (1-483) x BJ170744 (1-688)

QY 279 SerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgValLeuGlnTyrGln 298

Db 686 AGCAAGGACATACCTGGCCACAGTTGAGAAATAGACATCTCTGGAAATCCTCCATACCAG 627

Qy 299 HistYrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThrPheGlySerLeu 318

Db 626 CATCTGTTCTTCAAGGCTCTGTTATTTTTCGCCCGGTGGTAGTTGGCTCTTTTGGAGCTGG 567

Qy 319 LeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGlyThrVal 338

Db 566 AGATATACCTCTACAGCAGTGCTCTCACCTGTCGACAGGTGTTGGAGAGGGAAGTGT 507

Qy 339 AlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuProGlyValAlaLys 358

Db 506 CTGTTTCACTACTTTTGGTTCGTGGGACAGCGTGCTATCTTCTCCCTGGT---TGGAAG 450

Qy 359 ProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuGlyPheValPhe 378

Db 449 CCATTAGTATGATGGCGGTGACTGAGCTCATGTCCGSCATGCTGCTGGGCTTTCATTT 390

Qy 379 ThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheValArgAlaGln 398

Db 389 GTACTTAGCCACAATGGGATGGAGGTTTATAATTCGTCTAAAGAATTCGTGAGTGACAG 330

Qy 399 ValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeu 418

Db 329 ATCGTATCCACACCGGGATATCAAGGAACAATATTCACGACTGGTTCACCTGGTGCCCT 270

Qy 419 AspThrGlnIleGluHisLeuPheProThrMetProArgHisAsnTyrProLysIle 438

Db 269 AACAGCGCAATAGTGCATCATCTTTTCCCAACAATGCCAGGCATATTTAAACAAATA 210

Qy 439 AlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsnValSerVal 458

Db 209 GCACCTAGAGTGGAGGTGTTCTGTGAAGAAACACGGTCTGGTGACGAAGACGTATCTATT 150

Qy 459 ValGlyAlaSerValAlaValLysAlaLeuLysGluIleAlaAspGluAlaSerIle 478

Db 149 GCTACCGGCACCTTGCAAGGTTTGAAGACATTTGAAGGAAGTCGCG---GAGGCTGCGGCA 93

Qy 479 ArgLeuHisAla 482

Db 92 GAGCAGCATGCT 81

RESULT 4
BJ597842/c
LOCUS
DEFINITION
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pphn21ml1 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

BJ597842 728 bp mRNA linear EST 22-CCR-2003
BJ597842 normalized full length cDNA library, chloronemata,
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pphn21ml1 3', mRNA sequence.

BJ597842 GI:37839834
EST.
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 728)
Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H.,
Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K.,
Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
22709184
12808149
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-FLC phage vector (Carninci et al.
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector(5'- GAGAGAGAGGAGATCCAAACCCCTGGAGAGTTTCTTTTCTTTVN-3' was
used as a 1st 3' primer, and
5'-ggTTCGAGTCATCGTGTTCAGACAGCGATGACTCGAGAACCGNNNN-3' as 2nd
5'-hairpin primer, giving the following 5' boarder sequence,
AGGCCAAATCGCCGAGCTCGAATTCGTCGAGAACCG). cDNA instert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDATG medium for 13- 14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center
(http://www.brc.riken.go.jp/lab/epd/eng/index.html). The database
of Physcomitrella EST clones is available at the PHYSCObase
(http://moss.nibb.ac.jp).

Location/Qualifiers
1..728
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphn21ml1"
/tissue_type="mixture of chloronemata, caulonemata and
rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library,
chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Alignment Scores:
Pred. No.: 4.45e-64 Length: 728
Score: 617.00 Matches: 120
Percent Similarity: 73.10% Conservative: 24
Best Local Similarity: 60.91% Mismatches: 51
Query Match: 23.78% Indels: 2
DB: 12 Gaps: 2

US-09-980-468-2 (1-483) x BJ597842 (1-728)

Qy 286 ValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeuProLeu 305

Db 726 GTTGAGATAAGACATTTCTTGGAAATCTCTCAATACCAGCATCTGTCTTCATGGGTCTG 667

Qy 306 LeuPheMetAlaArgTyrSerTrpThrPheGlySerLeuLeuPheThrPheAsnProAsp 325

Db 666 TTATTTTTCGCCCGTGGTAGTTGGCTCTTTTGGAGCTGGAGATATACCTCTACAGCAGTG 607

Qy 326 LeuSerThrThrLysGlyLeuIleGluLysGlyThrValAlaPheHisTyrAlaTrpPhe 345

Db 606 CTCTCACCTGTCGACAGGTGTGTGGAGAAGGGAAGTCTGTCTGTCTTCTACTACTTTGGTTC 547

Qy 346 SerTrpAlaAlaPheHisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAla 365

Db 546 GTCGGACAGCGTGCTATCTCTCCCTGGT---TGGAAAGCCATTAGTATGGTGGTG 490

Qy 366 ThrGluLeuValAlaGlyLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLys 385

Db 489 ACTGAGCTCATGTCCGGCATGCTGTGGGCTTGTATTGTACTTAGCCACAATGGGATG 430

Qy 386 GluValTyrAsnGluSerLysAspPheValArgAlaGlnValIleThrThrArgAsnThr 405

Db 429 GAGGTTTATAATTCTCTAAAGAAATTCGTGAGTGCACAGATCGTATCCACCGGATATC 370

Qy 406 LysArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThrGlnIleGluHisHis 425

Db 369 AAAGGAAACATATTCAACGACTGGTTCACCTGGTGGCCTTAAACAGGCAATAGAGCATCAT 310

Qy 426 LeuPheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeu 445

Db 309 CTTTTCACCAATGCCAGGCAATAATTTAAACAAATAGCACCTAGATGGAGGTGTTTC 250

QY 446 CysLysLysHisGlyLeuGluTyrAspAsnValSerValValGlyAlaSerValAlaVal 465
|||||
Db 249 TGTAGAAACACGGTCTGGTGTACGAGACGTATCTATTGCTACCGGCACTTGCAAGGTT 190
|||||
QY 466 ValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeuHisAla 482
:::
Db 189 TTGAAGCATTTGAAGGAAGTCGCG---GAGCGTGGCGACAGCAGCATGCT 142
:::

RESULT 5
BJ599570/c
LOCUS
DEFINITION
697 bp mRNA linear EST 22-OCT-2003
BJ599570 normalized full length cDNA library, chloronemata,
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pphn26k05 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE
1 (bases 1 to 697)
AUTHORS
Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H.,
Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
Kohara, Y. and Hasebe, M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
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12808149
Contact: Tadasu Shin-i
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Tel: 81-559-81-6856
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that was in vivo excised from a l-FLC phage vector (Carninci et al.
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector(5'- GAGAGAGAGAGGATCCAAACCTGGAGAGTTTTTTTTTTTTTTVN-3' was
used as a 1st 3' primer, and
5'-ggTCTGgATCATGCTGTTCAGACAGCGATGACTCGAGAACCGNNNN-3' as 2nd
5'-hairpin primer, giving the following 5' boarder sequence,
AGGCCAAATCGCGGCTCGAATTCGTCGAGAACCG). cDNA instert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDATG medium for 13- 14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center
(http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database
of Physcomitrella EST clones is available at the PHYSCobase
(http://moss.nibb.ac.jp).

FEATURES
source
1. 697
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphn26k05"
/tissue type="mixture of chloronemata, caulonemata and
rhizoid-like protonemata"
/clone lib="normalized full length cDNA library,
chloronemata, caulonemata and rhizoid-like protonemata"
ORIGIN

Alignment Scores:
Pred. No.: 5.93e-60 Length: 697

Score: 583.00 Matches: 113
Percent Similarity: 72.19% Conservative: 22
Best Local Similarity: 60.43% Mismatches: 50
Query Match: 22.47% Indels: 2
DB: 12 Gaps: 2
US-09-980-468-2 (1-483) x BJ599570 (1-697)
QY 296 GlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTyrPhe 315
|||||
Db 696 CAATACCGCATCTGTTCTTCATGGGTCTGTATTTTCGCCCGTGGTAGTGGCTCTTT 637
|||||
QY 316 GlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLys 335
|||
Db 636 TGGAGCTGGAGATATACCTCTACAGCAGTGTCTCTACCTGTGACAGGTTGTTGGAGAAG 577
|||
QY 336 GlyThrValAlaPheHisTyrAlaTyrPheSerTyrAlaAlaPheHisIleLeuProGly 355
|||||
Db 576 GGAACCTGTTCTGTTTCACTACTTTTGGTTCGTCGGACAGCGTGTCTCTCCCTGGT 517
|||||
QY 356 ValAlaLysProLeuAlaTyrMetValAlaThrGluLeuValAlaGlyLeuLeuGly 375
|||||
Db 516 ---TGAAGCCATTAGTATGGATGGCGTGACTGAGCTCATGTCCGGCATGCTGCTGGGC 460
|||||
QY 376 PheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheVal 395
|||||
Db 459 TTTGTATTTGTACTTAGCCACATGGGATGGAGTTTATAATTGTTCTAAGAAATTGCTG 400
|||||
QY 396 ArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTyrPheAsnAspTyrPheThr 415
|||||
Db 399 AGTGCACAGATCGTATCCACACGGGATATCAAAGAAACATATTCAACGACTGGTCACT 340
|||||
QY 416 GlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHisAsnTyr 435
|||||
Db 339 GGTGGCCTTAACAGCGCAATAGAGCATCATCTTTCCCAACAATGCCAGGCATAATTA 280
|||||
QY 436 ProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsn 455
|||||
Db 279 AACAAATAGCACTAGAGTGGAGGTGTTCTGTGTAAGAAACACGGTCTGGTGTACGAGAC 220
|||||
QY 456 ValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAspGlu 475
|||||
Db 219 GTATCTATTGCTACCGGCACCTTGCAAGGTTTTGAAAGCATTGAAGGAAGTCGCG---GAG 163
|||||
QY 476 AlaSerIleArgLeuHisAla 482
|||||
Db 162 GCTCGCGCAGACGACGATGCT 142
|||||

RESULT 6
BJ604593/c
LOCUS
DEFINITION
698 bp mRNA linear EST 22-OCT-2003
BJ604593 normalized full length cDNA library, chloronemata,
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pphn31g10 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE
1 (bases 1 to 698)
AUTHORS
Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H.,
Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
Kohara, Y. and Hasebe, M.
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transcriptome and Arabidopsis thaliana: implication for land plant
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
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Contact: Tadasu Shin-i
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to Sali site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'- GAGAGAGAGAGGATCCAACTGGAGATTTTTTTTTTTTNN-3' was used as a 1st 3' primer, and 5'-gggtctcgagtcgctgttccagacagcgtatgactcgagAACGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGCGCGAGCTCGAATTCGTCGAGAACCG). cDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003). Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13- 14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCobase (<http://moss.rihb.ac.jp>).

FEATURES

source
1. 638
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphn31g10"
/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Alignment Scores:
Pred. No.: 5.95e-60 Length: 698
Score: 583.00 Matches: 113
Percent Similarity: 72.19% Conservative: 22
Best Local Similarity: 60.43% Mismatches: 50
Query Match: 22.47% Indels: 2
DB: 12 Gaps: 2

US-09-980-468-2 (1-483) x BJE04593 (1-698)

QY 296 GlnTyrGlnHisTyrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThrPhe 315
Db CAATACAGCATCTGTTCTTCATGGGTCTGTATTTCGCCCGTGGTAGTTGGCTCTT 637
QY 316 GlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLys 335
Db TGGAGTGGAGATATACCTCTACAGCAGTCTCTCACCTGTCTGACAGGTTGTGGAGAG 577
QY 336 GlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuProGly 355
Db GGAACGTCTGTTTCACTACTTTTGGTCTGTCGGGACAGCGTGCTATCTTCTCCCTGGT 517
QY 356 ValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuGly 375
Db ---TGAAGCCATTAGTATGGATGGCGGTGACTGAGCTCATGTCCGGCATGCTGTGGGC 460
QY 376 PheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheVal 395
Db TTTGTATTGTACTTAGCCACAATGGGATGGAGGTTTATAATTCTGTTAAAGATTCGTG 400
QY 396 ArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThr 415
Db AGTGCACAGATCGTATCCACACGGGATATCAAGGAACATATTACAGCACTGGTTCAC 340
QY 416 GlyGlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsnTyr 435

Db 339 GGTGGCCTTAACAGGCAATAGAGCATCATCTTTTCCCAACAATGCCAGCATATTTA 280
QY 436 ProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsn 455
Db AACAAATAGCACCTAGAGTGGAGGTTCTTGTAGAAACACGGTCTGTGTACGAAGAC 220
QY 456 ValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAspGlu 475
Db GTATCTATTGCTACCGGCACTTGCAGGTTTGAAGCATTTGAAGGAGTTCGCG---GAG 163
QY 476 AlaSerIleArgLeuHisAla 482
Db GCTGGCGGAGAGCAGCATGCT 142

RESULT 7

AY103762
LOCUS AY103762 PC0087385 mRNA sequence. linear HTC 16-OCT-2002
DEFINITION Zea mays
ACCESSION AY103762
VERSION AY103762.1 GI:21206840
KEYWORDS ETC.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

1 {bases 1 to 1764}
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tirgey,S.V.

AUTHORS

Maize Mapping Project/DuPont Consensus Sequences for Design of

TITLE

Overgo Probes

JOURNAL

Unpublished (2002)

REFERENCE

2 {bases 1 to 1764}

AUTHORS

Coe,E.H.

TITLE

Direct Submission

JOURNAL

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,

these are publicly available from ZmDB and may be found by BLAST

searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,

www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat

Schnable, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.

Location/Qualifiers

1. 1764
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:634923"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus

Library"

/note="this sequence is part of a project of EST

assemblies resulting from the application of public

contigs to seed DuPont contigs; this resource was

assembled by DuPont as part of a collaboration for the

overgo addressing of BACs in conjunction with the Maize

Mapping Project"

ORIGIN

Alignment Scores:
Pred. No.: 2.27e-57 Length: 1764
Score: 567.50 Matches: 149

Percent Similarity: 47.17% Conservative: 76

Best Local Similarity: 31.24% Mismatches: 230

Query Match: 21.87% Indels: 53

DB: 11 Gaps: 12

US-09-980-468-2 (1-483) x AY103762 (1-1764)

QY 31 ProThrLeuLysHisAlaLysLysValSerAlaGlnGlyLysThrAlaGlyGlnThrLeu 50

Db CCAATCAGCACCACCAAGGCGCATCCGAGCC-----ACGGCCGCGCAA---TGC 92

Gold gigapackaging extracts, propagated in XL-IBLue MRF cells and amplified. The library was excised by mass excision using Stratagene's Mass excision kit to infect SCLR cells with phagemids and ampicillin resistant transformants selected. Approximately 1,000,000 colonies were grown and recovered by using Qiagen midi prep kit.2 micro grams of plasmid DNA were used to transform DH10b cells by electroporation. Clones corresponding to abundant transcripts were identified by colony hybridization and eliminated from the library, be rearraying. This library is non-directionally cloned."

ORIGIN

Alignment Scores: Fred. No.: 8.59e-55 Length: 519 Score: 539.00 Matches: 104 Percent Similarity: 73.10% Conservative: 21 Best Local Similarity: 60.82% Mismatches: 44 Query Match: 20.77% Indels: 2 DB: 12 Gaps: 2

US-09-980-468-2 (1-483) x BQ040185 (1-519)

QY 312 SerTrpThrPheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGly 331
Db 4 AGTTGGCTCTTTGGAGCTGGAGATACCTCTACAGCAGTGTCTCACCTGTGACAGG 63
QY 332 LeuIleGlyLysGlyThrValAlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHis 351
Db 64 TTGTGGAGAGGAACTGTTCTGTTTCACTACTTTTGGTTCGTGGGACAGCGTGCTAT 123
QY 352 IleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGly 371
Db 124 CTTCTCCCTGGT---TGGAGCCCATTAAGTATGGATGGCGGTGACTGAGCTCATGTCGGC 180
QY 372 LeuLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSer 391
Db 181 ATGCTGCTGGGCTTTGTATTGCTACTAGCCCAATGGATGGAGTGGATTATATTCGTCT 240
QY 392 LysAspPheValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsn 411
Db 241 AAAGAATTGCTGAGTGCACAGATCGTATCCACACGGGATATCAAGGAAACATATTCAAC 300
QY 412 AspTrpPheThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetPro 431
Db 301 GACTGGTCACTGGTGGCCTTAACAGGCAAAATAGAGCATCATCTTTTCCCAACAATGCC 360
QY 432 ArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeu 451
Db 361 AGGCATAATTAAACAAATAGCACCTAGAGTGGAGTGTCTGTGAAGAACACGGTCTG 420
QY 452 GluTyrAspAsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGlu 471
Db 421 GTGTACGAAGACGTATCTATTGCTACCGGCACTTGCAAGGTTTGAAGCATTTGAAGAA 480
QY 472 IleAlaAspGluAlaSerIleArgLeuHisAla 482
Db 481 GTCCGG---GAGGCTGGGGCAGAGCAGCATGCT 510

RESULT 9 AK076485 LOCUS AK076485 2272 bp mRNA linear HTC 18-SEP-2003 DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833423E24 product:unclassifiable, full insert sequence.

ACCESSION AK076485 VERSION AK076485.1 GI:26096835 KEYWORDS HTC; CAP trapper. SOURCE Mus musculus (house mouse) ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 REFERENCE

AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE

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Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1993) 99279253 10349636 2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159 3

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861 4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2272)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Kashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katch,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome-gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

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genomic survey sequence.
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AY418548
VERSION
AY418548.1
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REFERENCE
1 (bases 1 to 1335)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1335)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
```


Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-MOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
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HTC; CAP trapper.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
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AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
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AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
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JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374

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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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PUBMED
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THE RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
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US-09-980-468-2 (1-483) x AK083959 (1-3318)

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QY 408 GlyTyrPheAsnAspTrpPheThrGlyGlyLeuAspThrGlnIleGluHisLeuPhe 427

Db 365 AACATATTCAACGACTGGTTCACTGGTGGCCTTAACAGGCAATAGAGCATCATCTTTC 306

QY 428 ProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCysLys 447

Db 305 CCAACAATGCCAGGCATAATTATAACAAATAGCACCTAGAGTGGAGGTGTCTGTAAAG 246

QY 448 LysHisGlyLeuGluTyrAspAsnValSerValValGlyAlaSerValAlaValValLys 467

Db 245 AAACACGGCTGGTGTACGAAGACGTATCTATTGCTACCGGCACCTTGCAGGTTTGAAA 186

QY 468 AlaLeuLysGluIleAlaAspGluAlaSerIleArgLeuHisAla 482

Db 185 GCATTGAAGGAAGTCGCG--GAGGCTGCGGCAGCAGCATGCT 144

RESULT 13

AK080414

LOCUS

DEFINITION

AK080414 1689 bp mRNA linear HTC 19-SEP-2003

Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730007D17 product:fatty acid desaturase 3, full insert sequence.

AK080414

AK080414.1 GI:26348536

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

AUTHORS

TITLE

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1993)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

AUTHORS

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

20499374

PUBMED

11042159

REFERENCE

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

AUTHORS

TITLE

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE

20530913

PUBMED

11076861

REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

AUTHORS

TITLE

Functional annotation of a full-length mouse cDNA collection

JOURNAL

Nature 409, 685-690 (2001)

MEDLINE

11076861

PUBMED

11076861

REFERENCE

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

AUTHORS

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

MEDLINE

11076861

PUBMED

11076861

REFERENCE

6

(bases 1 to 1689)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

FEATURES

source

1..1689

Location/Qualifiers

organism="Mus musculus"

mol_type="mRNA"

strain="C57BL/6J"

db_xref="FANTOM DB:A730007D17"

db_xref="MGI:2407629"

db_xref="taxon:10090"

clone="A730007D17"

tissue_type="cerebellum"

clone_lib="RIKEN full-length enriched mouse cDNA library"

dev_stage="7 days neonate"

37..1386

note="unnamed protein product; fatty acid desaturase 3 (MGD|MGI:1928740, GB|NM_021890, evidence: BLASTN, 99%, match=1700)

putative"

codon_start=1

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db_xref="GI:26348537"

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ORIGIN

Alignment Scores:

Pred. No.:	4.18e-51	Length:	1689
Score:	516.00	Matches:	138
Percent Similarity:	47.39%	Conservative:	71
Best Local Similarity:	31.29%	Mismatches:	166
Query Match:	19.88%	Indels:	66
DB:	11	Gaps:	17

US-09-980-468-2 (1-483) x AK080414 (1-1689)

QY 68 ValAlaSerHisAspArgProGlyAspCysTyrMetIleValLysGluLysValTyrAsp 87

Db 130 ATCCGCCAGCATGACCTACACGGCGACAGTGGCTGGTTCATCGAGCGCGTGTCTACGAC 189

QY 88 IleSerArgPheAlaAspAspHisProGlyGlyThr---ValIleSerThrTyrPheGly 106

Db 190 ATCAGCCGCTGGGCACACGGCGACCCAGGGGGTAGCCGCTCATCGGCCACACCGGTGCG 249

QY 107 ArgAspGlyThrAspValPheAlaThrPheHisProProAlaAlaTrp-----LysGln 124
Db 250 GAGGACGCCAGGATGCCTCCACGCCCTCCACCAAGATCTCCATTTTGTGCGCAAGTTC 309
QY 125 LeuAsnAspTyrTyrIleGlyAspLeuAlaArgGluGluProLeuAsp----- 140
Db 310 CTGAACCCCTGTGATTGGAGAGCTAGCCCCAGAGGAACCCAGCCAGGATGGAGCTCAG 369
QY 141 -----GluLeuLeuLysAspTyrArgAspMetArgAlaGluPheValArgGluGlyLeu 158
Db 370 AATGCCAGCTGATCGAGGACTTCCGAGGCTTGCGCCAGGCAGCTGAACATGAAGCTG 429
QY 159 PheLysSerSerLysAlaTrpPhe---LeuLeuGlnThrLeuIleAsnAlaAlaLeuPhe 177
Db 430 TTTGAAGCTGATAGCACTTTCTTTGCACCTCTGCTGGGCCACTCTCTGGCTATGGAGTTG 489
QY 178 AlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleValLeuSerAla 197
Db 490 TTEGCTTGGCTTATCATCTACCTCTTGGGCCCTGGCTGGGTGCCAGTATCCTTGTGCC 549
QY 198 SerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPheLeuHisGln 217
Db 550 CTGATCCTGGCCATCTCTCAGGCCAGTGTGGTGTCTGCAACATGATCTAGGTCTATGCT 609
QY 218 GlnValPheGlu-----AsnArgThrAlaAsnSerPhePheGlyTyrLeuPhe 233
Db 610 TCCATCTTCACTAAGTCCAGGTGAACCATGTGSCCCAGCAGTTC-----GTGATG 660
QY 234 GlyAsnCysValLeuGlyPheSerValSerTrpArgThrLysHisAsnIleHisHis 253
Db 661 GGGCAG---TTGAAGAGCTTTTCGGCCCACTGGTGGGAATTTCCGCCACTTCCAGCACCAT 717
QY 254 ThrAlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeu 273
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Db 763 CCTGTCTTCTCTCGGGGAGTCACTCTGGGAGTATGGCAAGAAACGC-----AGA 816
QY 294 ValLeuGlnTyrGlnHis-----TyrMetIleLeu-----ProLeuLeuPhe 307
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QY 316 GlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLys 335
Db 934 ---GACTTGTCTGG----- 945
QY 336 GlyThrValAlaPheHisTyrAlaTrpPhe---SerTrpAlaAlaPheHisIleLeuPro 354
Db 946 ---GCTGCCAGTTTCTACTCCCGCTTTTCTTGTCTCTACTCTCCCTTCTAT----- 993
QY 355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374
Db 994 GGTGCCACTGGGACACTGCTCTCTTTTGTCTGTGAGGCTGGAGAGCCACTGTTTC 1053
QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSer---LysAsp 393
Db 1054 GTGTGGATCAGCAGATGAACACATCCCCAGGAGATGGCCATGAAAGCATCGGGAC 1113
QY 394 PheValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrp 413
Db 1114 TGGCAAGCTCTCAGCTGGCAGCCACCTGCAATGTGGAACCTTCTCTTCAATGACTGG 1173
QY 414 PheThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHis 433
Db 1174 TTCAGCGGGCACCTCAATTCCAGATTGAGCACCACCTCTTCCCCACGATGCCAAGSCAC 1233
QY 434 AsnTyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyr 453

Db 1234 AACTACCGGAGGTGGCCCCCTTGGTCAAGCGCTTCTGCGCAAGCACGGCTACTACTAC 1293
QY 454 AspAsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAla 473
Db 1294 GAGGTGAAGCCTTCTCACCCTCTGTTGGATATCATCGGTCCCTGAAGAAGTCTGGC 1353
QY 474 Asp 474
Db 1354 GAC 1356
RESULT 14
AK029318
LOCUS
DEFINITION
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832423A09 product:fatty acid desaturase 3, full insert sequence.
AK029318
VERSION AK029318.1 GI:26325277
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
REFERENCE
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
REFERENCE
4 The RIKEN Genome Exploration Research Group Phase II Team and the RIKEN Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
REFERENCE
5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
REFERENCE
6 (bases 1 to 3129)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda,Y., Tanaka,T., Tomaru,A., Taya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source

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CDS

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437 TTTGAAGCTGATACCACTTTCTTTGGCACTCTGCTGGGCCACATCTCTGGCTATGGAGTTG 496
178 AlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleValLeuSerAla 197
497 TTGGCCTGGCTTATCATCTACCTCTTGGGCCCTGGCTGGGTGTCCAGTATCTCTGCTGCC 556
198 SerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPheLeuHisGln 217
557 CTGATCCTGGCCATCTCTCAGGCCCATGTGCTGTGTCTGCAACATGATCTAGGTCTGCT 616
218 GlnValPheGlu-----AsnArgThrAlaAsnSerPhePheGlyTyrLeuPhe 233
617 TCCATCTTCACTAAGTCCAGGTGAACCATGTGGGCCAGCAGTTC-----GIGATG 667
234 GlyAsnCysValLeuGlyPheSerValSerTyrTrpArgThrLysHisAsnIleHisHis 253
668 GGGCAG--TTGAAGGCTTTTCCGCCCACTGGTGAATTTCCGCCACTTCCAGCACCAT 724
254 ThrAlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeu 273
725 GCCAAACCCAAACATCTCCACAA-----GACCCAGATGTGACTGTCCGCA 769
274 ProIleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArg 293
770 CCTGTCTTCTCCTGGGGAGTCACTGTGGAGTATGGCAAGAAACGC-----AGA 823
294 ValLeuGlnTyrGlnHis-----TyrMetIleLeu-----ProLeuLeuPhe 307
824 TACCTGCCCTACAACCCAGCATCTATACTTCTTCTGATTTGCTGCTGCTGCTCACC 883
308 MetAlaArgTyr-----SerTrpThrPhe 315
884 TTGGTGAACCTTTGAAGTTGAAATCTGGGTACATGCTGTGTGCTGCTGCTGCTGCTGCTG 940
316 GlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLys 335
941 ---GACTTGTGTGG----- 952
336 GlyThrValAlaPheHisTyrAlaTrpPhe---SerTrpAlaAlaPheHisIleLeuPro 354
953 ---GCTGCCAGTTTCTACTCCCGCTTTTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1000
355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374
1001 GGTGCCACTGGGACACTGCTCTCTTTGTTGCTGTCTGCTGCTGGAGAGCCACTGGTTC 1060
375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSer---LysAsp 393
1061 GTGTGGATCAAGCAGATGAACACATCCCAAGGAGATGGCCATGAAAGCATCGGGAC 1120
394 PheValArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrp 413
1121 TGGGCAAGCTCTCAGCTGGCACCCACCTGTCAATGTGGAACCTTCGCTCTTCTTCTTCTTCT 1180
414 PheThrGlyGlyLeuAspThrGlnIleGluHisHisLeuPheProThrMetProArgHis 433
1181 TTCAGCGGGCACCTCAATTTCCAGATTGAGCACCACCTTTCCTCCACGATGCCAAGGCAC 1240
434 AsnTyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyr 453
1241 AACTACCGGAGGGTGGCCCCCTGGTCAAGGCGTTCTCGCCCAAGCAGCGCTACACTAC 1300

ORIGIN

Alignment Scores:
Pred. No.: 2,1e-50 Length: 3129
Score: 514.00 Matches: 138
Percent Similarity: 47.39% Conservative: 71
Best Local Similarity: 31.29% Mismatches: 166
Query Match: 19.81% Indels: 66
DB: 11 Gaps: 17
US-09-980-468-2 (1-483) x AK329318 (1-3129)
QY 68 ValAlaSerHisAspArgProGlyAspCysTyrMetIleValLysGluLysValTyrAsp 87
Db 137 ATCCGCCAGCATGACCTACAGGCGACAAAGTGGTGGTTCATCGAGCGCCGCTGTCTACGAC 196
QY 88 IleSerArgPheAlaAspAspHisProGlyGlyThr---ValIleSerThrThrPheGly 106
Db 197 ATCAGCCGCTGGGCACAGCGGCACCCAGGGGGTAGCGGCCTCATCGGCCACCGGTGCG 256
QY 107 ArgAspGlyThrAspValPheAlaThrPheHisProProAlaAlaTrp-----LysGln 124
Db 257 GAGGACGCCACGGATGCTTCCACGCCCTTCCACCAAGATCTCCATTTTGTGGCGAAGTTC 316

Qy 454 AspAsnValSerValValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAla 473
Db 1301 GAGGTGAAGCCTTCTCCTCACCGCTCTGGTGGATATCATCGGTCCTGAGAGAGTCTGGC 1360
Qy 474 Asp 474
Db 1361 GAC 1363

RESULT 15
AY418550 1335 bp DNA linear GSS 17-DEC-2003
LOCUS Mus musculus FADS2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY418550
VERSION AY418550.1 GI:39774510
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1335)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..1335
/organism="Mus musculus"
/mol_type="genomic DNA"
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/gene="FADS2"
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ORIGIN
Alignment Scores:
Pred. No.: 1.09e-49 Length: 1335
Score: 503.00 Matches: 137
Percent Similarity: 46.11% Conservative: 82
Best Local Similarity: 28.84% Mismatches: 162
Query Match: 19.38% Indels: 94
DB: 29 Gaps: 20

US-09-980-468-2 (1-483) x AY418550 (1-1335)

Qy 42 GlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSerValGlnAspLysProGly 61
Db 19 CAGGGAGAG-----GGGAGCACCAGCGCCAGGCTCCGATGCCC----- 57

Qy 62 ThrTyrSerLeuAlaAspValAlaSerHisAspArgProGlyAspCysTrpMetIleVal 81
Db 58 ACCTCCGTTGGGAGGAGATTCAGAGCACACACCTGGCCACCGACCGGTGGCTCGTCATC 117

Qy 82 LysGluLysValTyrAspIleSerArgPheAlaAspAspHisProGlyGly---ThrVal 100
Db 118 GACCGCAAGGTCTACACAGTTACCAATGGTCCCGCGGCACCGCGGGGCCACCGTGTC 177

Qy 101 PheSerThrTyrPheGlyArgAspGlyThrAspValPheAlaThrPheHisProAla 120
Db 111

Db 178 ATCGGACACTATTTCGGGAGAGATGCTACGGATGCCCTCCGTCCTTCATCTGGACCTG 237
Qy 121 AlaTrp-----LysGlnLeuAsnAspTyrTyrIleGlyAspLeuAlaArgGluPro 138
Db 238 GACTTCGTGGCAAGTTCCTTGAGCCCTGCTGATTTGGTGGCTGGCCCAAGAGAGCCC 297
Qy 139 ---LeuAsp-----GluLeuLeuLysAspTyrArgAspMetArgAlaGlu 152
Db 298 AGCCTGGACCGTGGCAAAAGCTCTCAGATCACCGAGGACTTCAGGGCCCTGAAGAAGACT 357
Qy 153 PheValArgGluGlyLeuPheLysSerSerLysAlaTrpPheLeuLeuGlnThrLeuIle 172
Db 358 GCTGAGGACATGACCTCTTCAAAACCAACCAACCTGTTCTTCTTCTC-----CTCCTG 411
Qy 173 AsnAlaIleLeuPheAlaAlaSerIleAla-----ThrIleCysTyrAspLysSerTyr 190
Db 412 TCCACATCATCGTCATGGAAAGCCTTSCCTGGTTTCATCTCTCGTACTTCGGCACTGGC 471
Qy 191 Trp---AlaIleValLeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrp 209
Db 472 TGGATTCTTACCCTCGTCACASCCTTTGTCTCTCGTACCTCTCAGGCCCAAGCTGGATGG 531
Qy 210 LeuAlaHisAspPheLeuHisGlnGlnValPheGlu-----AsnArgThrAla 225
Db 532 CTGCAACATGACTATGGCCACCTTTCTGTCTATAAGAAATCCATATGGAACCACTGTGC 591
Qy 226 AsnSerPhe---PheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTrp 244
Db 592 CACAAGTTTGTCATTGGCCACTTA-----AAGGGTGCCTCAGCCCACTGG 636
Qy 245 TrpArgThrLysHisAsnIleHisHisThrAlaProAsnGluCysAspGlnGlnTyrThr 264
Db 637 TGAACACCAACCGACATTTCCAAACCACTATGCCAAGCCCAACATCTTCCACAAG----- 687
Qy 265 ProLeuAspGluAspIleAspThrLeuProIleAlaTrpSerLysGluIleLeuAla 284
Db 688 -----GACCCGACATAAAGAGCCTGTCATGTGTGTGTCTTGGC---GAGTGGCAGCCC 738
Qy 285 ThrValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyr----- 300
Db 739 CTTGAGTATGGCAAGAAGAAGCTGAATACCTGCCTTACCAACCAACCAAGCATGAACTTC 798
Qy 301 -----MetIleLeuProLeuLeuPhe----- 307
Db 799 TTCCTGATCGGACCGCCGCTGCTCATCCCTATGCTTCCAGTACCAGATCATCATGACA 858
Qy 308 ---MetAlaArgTyrSerTrpThr-----PheGlySerLeu 318
Db 859 ATGATCAGCCCGCAGGACTGGTGGACTTGGCTTGGGCCATCAGCTACTATATGCGTTTC 918
Qy 319 LeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGlyThrVal 338
Db 919 TTCTACACCTACATCCCTTTCTACGGCATCTTGGGAGCCCTGGTTTCTCAACTTATC 978
Qy 339 AlaPhe---HisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuProGlyValAla 357
Db 979 AGGTTCTCTGGAGAGCCACTGGTTGTGTGG----- 1008
Qy 358 LysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuGlyPheVal 377
Db 1009 -----GTC 1011
Qy 378 PheThrLeuSerHisAsnGlyLysGluVal---TyrAsnGluSerLysAspPheValArg 396
Db 1012 ACACAGATGAACCACTTGTTCATGGAGATTGATCTGTGATCCTACCGGACTGGTTGAGC 1071
Qy 397 AlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThrGly 416
Db 1072 AGCCAGCTGGCAGCCACCTGCAATGTGGAGCAGTCTCTTCAATGACTGGTTGAGCGGG 1131
Qy 417 GlyLeuAspThrGlnIleGluHisLeuPheProThrMetProArgHisAsnTyrPro 436
Db 1132 CACCTCAATTTCAGATTGAGCACCACCTCTTCCCCACTATGCCACGTCACCAACCTGCAC 1191

Qy	437	LysIleAlaProGlnValGluAlaLeuCysLysLysHisGlyLeuGluTyrAspAsnVal	456
Db	1192	AAAGATTGCCCCCACTGGTGAAGTCTCTCTGCGCCCAAGCATGGCATTTGAATACCCAGGAGAAG	1251
Qy	457	SerValValGlyAlaSerValAlaValValLysAlaLeuLysGlu	471
Db	1252	CCGTTGCTGAGGGCCCTGATCGACATTGTGAGTTTCACTGAAGAAG	1296

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Job time : 3775 secs